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(54) Title: NUCLEIC ACIDS ENCODING PROTEIN KINASES

(57) Abstract: Nucleic acids encoding protein kinases are disclosed, and methods of using same.



WO 03/000901 A2

NUCLEIC ACIDS ENCODING PROTEIN KINASES

RELATED APPLICATIONS

5 This application claims the benefit of and priority to U.S. Provisional Application 60/301,098, filed June 26, 2001 and to U.S. Provisional Application 60/332,870, filed November 6, 2001, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

10 Protein kinases are enzymes that catalyze the phosphorylation of target protein substrates. The phosphorylation is usually a transfer reaction of a phosphate group from ATP to the protein substrate.

At least 400 enzymes have been identified as protein kinases. The specific structure in the target substrate to which the phosphate is transferred is frequently a
15 tyrosine, serine or threonine residue, and such protein kinase enzymes are commonly referred to as tyrosine kinases or serine/threonine kinases. Another class of protein kinases phosphorylates histidine residues. Most protein kinases recognize a simple amino acid motif associated with a nearby residue.

The phosphorylation reactions, and counteracting phosphatase reactions, are
20 involved in countless cellular processes that underlie responses to diverse intracellular signals (typically mediated through cellular receptors), regulation of cellular functions, and activation or deactivation of cellular processes. A cascade of protein kinases often participate in intracellular signal transduction and are necessary for the realization of these cellular processes. Because of their ubiquity in
25 these processes, the protein kinases can be found as an integral part of the plasma membrane or as cytoplasmic enzymes or localized in the nucleus, often as components of enzyme complexes. In many instances, these protein kinases are an essential element of enzyme and structural protein complexes that determine where and when a cellular process occurs within a cell.

30 Protein kinases are regulated by a variety of mechanisms. Some protein kinases are constitutively active, while others are activated by the binding of a messenger (cAMP-dependent protein kinase, *e.g.*, protein kinase A; cGMP-dependent protein kinase; protein kinase C). Some are activated by calcium and calmodulin (*e.g.*, Ca^{2+} /calmodulin-dependent protein kinase II, phosphorylase
35 kinase, myosin light chain kinase, elongation factor 2 kinase). Protein kinases that

are activated by such a messenger tend to regulate most or all of the intracellular responses to the messenger.

Other protein kinases are activated by an extracellular signal, and are also called the receptor protein kinases (*e.g.*, polypeptide hormones receptors, growth factors, insulin, epidermal growth factor, platelet-derived growth factor). The catalytic domain of such protein kinases is also the cytoplasmic domain of a transmembrane receptor, the the extracellular domain binds an extracellular messenger. Binding to the domain activates the protein kinase inside the membrane.

Finally, some protein kinases are in turn regulated by other protein kinases, and multiple such relationships between protein kinases can exist, forming a protein kinase cascade, in which each protein kinase phosphorylates the next. Such kinases include, *e.g.*, cAMP-dependent protein kinase, AMP-activated protein kinase, MAP kinase kinase kinase, MAP kinase kinase, MAP kinase and S6 kinase.

SUMMARY OF THE INVENTION

The present invention relates to human protein kinase genes, particularly nucleic acids comprising protein kinase genes, and the amino acids encoded by such nucleic acids. These genes are shown in Tables I and II and the sequence listing. In Tables I and II, each kinase entry lists the name (*e.g.*, "MOOSE03013"), the University of California at Santa Cruz contig designation from which the sequence was analyzed (*e.g.*, "ctg14435"), and the exon locations (*e.g.*, "1134827 . . 1135076, . .").

Sub-family information on the sequences is shown in Table III. For each sequence, the following information is provided: the University of California at Santa Cruz contig designation from which the sequence was analyzed (*e.g.*, "ctg14435"), the name (*e.g.*, "MOOSE03013"), and the subfamily to which the sequence appears to belong. The assignments were made on the basis of the best E-value with which the sequence aligned.

In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), as shown in Tables I and II, and the complements thereof. The invention further relates to a nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), as shown in Tables I and II, and the complements thereof. The invention additionally relates to isolated nucleic acid molecules (*e.g.*, cDNA

molecules) encoding a protein kinase polypeptide (*e.g.*, encoding a polypeptide selected from the group consisting of SEQ ID NOs: 1-80 (even numbers).

The invention further provides a method for assaying a sample for the presence of a nucleic acid molecule comprising all or a portion of a protein kinase in a sample, comprising contacting said sample with a second nucleic acid molecule comprising a nucleotide sequence encoding a protein kinase polypeptide (*e.g.*, one of SEQ ID NOs: 1-80 (even numbers, or the complement of one of SEQ ID NOs: 1-80 (even numbers); a nucleotide sequence encoding one of SEQ ID NOs: 1-80 (odd numbers), or a fragment or derivative thereof, under conditions appropriate for selective hybridization. The invention additionally provides a method for assaying a sample for the level of expression of a protein kinase polypeptide, or fragment or derivative thereof, comprising detecting (directly or indirectly) the level of expression of the protein kinase polypeptide, fragment or derivative thereof.

The invention also relates to a vector comprising an isolated nucleic acid molecule of the invention operatively linked to a regulatory sequence, as well as to a recombinant host cell comprising the vector. The invention also provides a method for preparing a polypeptide encoded by an isolated nucleic acid molecule described herein (a protein kinase polypeptide), comprising culturing a recombinant host cell of the invention under conditions suitable for expression of said nucleic acid molecule.

The invention further provides an isolated polypeptide encoded by isolated nucleic acid molecules of the invention (*e.g.*, protein kinase polypeptide), as well as fragments or derivatives thereof. In a particular embodiment, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-80 (even numbers). The invention also relates to an isolated polypeptide comprising an amino acid sequence which is greater than about 90 percent identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-80 (even numbers), preferably about 95, 96, 97, 98 or 99 percent identical.

The invention also relates to an antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of the invention, as well as to a method for assaying the presence of a polypeptide encoded by an isolated nucleic acid molecule of the invention in a sample, comprising contacting said sample with an antibody which specifically binds to the encoded polypeptide.

The invention further relates to methods of diagnosing a predisposition to a condition mediated by a protein kinase. The methods of diagnosing such a predisposition in an individual include detecting the presence of a mutation in a

protein kinase, as well as detecting alterations in expression of a protein kinase polypeptide, such as the presence of different splicing variants of protein kinase polypeptides. The alterations in expression can be quantitative, qualitative, or both quantitative and qualitative.

5 The invention additionally relates to an assay for identifying agents that alter (*e.g.*, enhance or inhibit) the activity or expression of one or more protein kinase polypeptides. For example, a cell, cellular fraction, or solution containing a protein kinase polypeptide or a fragment or derivative thereof, can be contacted with an agent to be tested, and the level of protein kinase polypeptide expression or activity
10 can be assessed. The activity or expression of more than one protein kinase polypeptide can be assessed concurrently (*e.g.*, the cell, cellular fraction, or solution can contain more than one type of protein kinase polypeptide, such as different splicing variants, and the levels of the different polypeptides or splicing variants can be assessed).

15 In another embodiment, the invention relates to assays to identify polypeptides which interact with one or more protein kinase polypeptides. In a yeast two-hybrid system, for example, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also a protein kinase polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a
20 polypeptide which potentially may interact with the protein kinase polypeptide, splicing variant, or fragment or derivative thereof (*e.g.*, a protein kinase polypeptide binding agent or receptor). Incubation of yeast containing both the first vector and the second vector under appropriate conditions allows identification of polypeptides
25 which interact with the protein kinase polypeptide or fragment or derivative thereof, and thus can be agents which alter the activity of expression of a protein kinase polypeptide.

 Agents that enhance or inhibit protein kinase polypeptide expression or activity are also included in the current invention, as are methods of altering
30 (enhancing or inhibiting) protein kinase polypeptide expression or activity by contacting a cell containing protein kinase and/or polypeptide, or by contacting the protein kinase polypeptide, with an agent that enhances or inhibits expression or activity of protein kinase or polypeptide.

 Additionally, the invention pertains to pharmaceutical compositions
35 comprising the nucleic acids of the invention, the polypeptides of the invention, and/or the agents that alter activity of protein kinase polypeptide. The invention

further pertains to methods of treating conditions mediated by protein kinases, by administering protein kinase therapeutic agents, such as nucleic acids of the invention, polypeptides of the invention, the agents that alter activity of protein kinase polypeptide, or compositions comprising the nucleic acids, polypeptides, and/or the agents that alter activity of protein kinase polypeptide.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to nucleic acids comprising protein kinases, and the protein kinase amino acids encoded by those nucleic acids.

Protein kinases are involved in regulation of cellular functions, and activation or deactivation of cellular processes, and many of the cellular processes in response to intracellular signals. Cascades of protein kinases often participate in intracellular signal transduction and are necessary for the realization of these cellular processes.

Protein kinases are the major modes through which extracellular signal molecules produce intracellular effects. They are also involved in stress responses, and protect the cell against changes in metabolite levels that would otherwise be toxic to the cell. They are also the major way in which mechanisms such as DNA synthesis and mitosis are timed.

The receptor tyrosine kinases comprise a large family of transmembrane receptors with diverse biological activities. At least nineteen distinct receptor tyrosine kinase subfamilies have been identified. This family includes receptors that are crucial for the growth and differentiation of a variety of cell types (Yarden and Ullrich, *Ann. Rev. Biochem.* 57:433-478 (1988); Ullrich and Schlessinger, *Cell* 61:243-254 (1990)). The intrinsic function of receptor tyrosine kinases is activated upon ligand binding, which results in phosphorylation of the receptor and multiple cellular substrates, and subsequently in a variety of cellular responses (Ullrich & Schlessinger, *Cell* 61:203-212 (1990)). Thus, receptor tyrosine kinase-mediated signal transduction is initiated by extracellular interaction with a specific growth factor (ligand), typically followed by receptor dimerization, stimulation of the intrinsic protein tyrosine kinase activity and receptor trans-phosphorylation. Binding sites are thereby created for intracellular signal transduction molecules and lead to the formation of complexes with a spectrum of cytoplasmic signaling molecules that facilitate the appropriate cellular response (*e.g.*, cell division, differentiation, metabolic effects, changes in the extracellular microenvironment).

Several receptor tyrosine kinases such as FGFR-1, PDGFR, TIE-2 and c-Met, and growth factors that bind them, have been suggested to play a role in

angiogenesis, although some may promote angiogenesis indirectly (Mustonen and Alitalo, *J. Cell Biol.* 129:895-898 (1995)). One such receptor tyrosine kinase, known as fetal liver kinase 1 (FLK-1), is a member of the type III subclass of RTKs. An alternative designation for human FLK-1 is a kinase insert domain-containing receptor (KDR) (Terman *et al.*, *Oncogene* 6:1677-83 (1991)). Another alternative designation for FLK-1/KDR is vascular endothelial cell growth factor receptor 2 (VEGFR-2), since it binds VEGF with high affinity. The murine version of FLK-1/VEGFR-2 has also been called NYK (Oelrichs *et al.*, *Oncogene* 8(1):11-15 (1993)). DNAs encoding mouse, rat and human FLK-1 have been isolated, and the nucleotide and encoded amino acid sequences reported (Matthews *et al.*, *Proc. Natl. Acad. Sci. USA* 88:9026-30 (1991); Terman *et al.*, 1991, *supra*; Terman *et al.*, *Biochem. Biophys. Res. Comm.* 187:1579-86 (1992); Millauer *et al.*, *Cell* 72:835-846 (1993)). Numerous studies such as those reported in Millauer *et al.*, *supra*, suggest that VEGF and FLK-1/KDR/VEGFR-2 are a ligand-receptor pair that play an important role in the proliferation of vascular endothelial cells, and formation and sprouting of blood vessels, termed vasculogenesis and angiogenesis, respectively.

Protein tyrosine kinases catalyse the phosphorylation of specific tyrosine residues in cellular proteins, and this post-translational modification of these substrate proteins, which can be enzymes themselves, acts as a molecular switch regulating cell proliferation, activation or differentiation (for review, see Schlessinger and Ullrich, *Neuron* 9:383-391 (1992)). Aberrant or excessive protein tyrosine kinase activity has been observed in many disease states including benign and malignant proliferative disorders as well as diseases resulting from inappropriate activation of the immune system (*e.g.*, autoimmune disorders), allograft rejection, and graft vs. host disease. In addition, endothelial-cell specific receptor protein tyrosine kinases such as KDR and Tie-2 mediate the angiogenic process, and are thus involved in supporting the progression of cancers and other diseases involving inappropriate vascularization. Angiogenesis-mediated diseases include, but are not limited to, cancers, solid tumors, blood-born tumors (*e.g.*, leukemias), tumor metastasis, benign tumors (*e.g.*, hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas), infantile hemangiomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases (*e.g.*, diabetic retinopathy, retinopathy of prematurity, choroidal neovascularization due to age-related macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis), Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularization, telangiectasia, hemophiliac joints, angiofibroma, and wound granulation.

Some intracellular protein kinases specifically interact with various members of the G protein-coupled receptor superfamily, and are able to desensitize them and thereby weaken the signal or prevent it from being effected. The G protein-coupled receptors are involved in the transmission of signals that originate from low molecular weight ligands such as adrenaline or from peptide ligands such as chemokines and a variety of hormones such as melanocyte stimulating hormone (MSH). So far, six of these kinases have been discovered (GRK1 through GRK6). Some of the GRKs are restricted to a small number of tissues (*e.g.*, GRK-1), while GRK2 and 3, known also as β ARK1 and β ARK2, are ubiquitously expressed. A comprehensive review is provided, for example, by M. Bunemann and M.M. Hosey, "G-Protein Coupled Receptor Kinases as Modulators of G-Protein Signalling," *J. of Physiology, Vol. 517(1):5-23* (1999). Methods and substances that modulate (increase or decrease) the function of 7TM receptors could be used to treat a wide variety of diseases and conditions associated with 7TM receptor function. G protein-coupled receptors, for instance, are involved in an enormous range of biological processes, and have been found to regulate such processes as hydrolysis of plasma membrane phospholipids, the K^+ and Ca^{2+} ion channels, yeast mating signals, the signaling by cholera and pertussis toxins, and proliferation in some cancers (*e.g.*, pituitary, adrenal, ovarian). Many drugs bind to a G protein-coupled receptor and either produce a response or block the actions of the normal signal. The GPCR superfamily includes the receptors for many important signaling pathways, including, but not limited to, hormone receptors, growth factors, viral receptors, neuroreceptors, etc., such as acetylcholine, adrenocorticotropin (ACTH), adenosine, α -adrenergic receptors, β -adrenergic receptors, angiotensin, bombesin, bradykinin, C5a, calcitonin, cAMP, cannabinoid, C-C chemokine, cholecystokinin/gastrin (CCK/gastrin), cytomegalovirus, dopamine, endothelial differentiation gene-1, endothelin, formyl peptide, glutamate (metabotropic), gonadotropin-releasing hormone, growth hormone-releasing hormone, histamine, 5-hydroxytryptamine, interleukin-8, kinin, luteinizing hormone/follicle-stimulating hormone/thyroid-stimulating hormone (LH/FSH/TSH), mas, melanocortin, muscarinic, neuropeptide Y, neurotensin, odorant, opioid, opsins, parathyroid hormone, platelet-activating factor (PAF), prolactin, prostaglandin E, rhodopsins, secretin, serotonin, somatostatin, tachykinin, taste, testis specific, thrombin, thromboxane A₂, thyrotropin-releasing hormone (TRH), tyramine/octopamine, vasoactive intestinal peptide (VIP), vasopressin, viral and yeast mating factor.

These receptors are involved in the treatment of infections and various diseases and conditions, including, but not limited to, bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2; cancers; diabetes; asthma; Parkinson's disease; both acute and congestive heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcers; asthma; allergies; benign prostatic hypertrophy (benign prostatic hyperplasia); chronic renal failure; renal disease; impaired glucose tolerance; seizure disorder; depression; anxiety; obsessive compulsive disorder; affective neurosis/disorder; depressive neurosis/disorder; anxiety neurosis; dysthymic disorder; behavior disorder; mood disorder; schizophrenia; psychosexual dysfunction; sex disorder; sexual disorder; disturbed biological and circadian rhythms; feeding disorders, such as anorexia, bulimia, cachexia, and obesity; Cushing's syndrome/disease; basophil adenoma; prolactinoma; hyperprolactinemia; hypopituitarism; hypophysis tumor/adenoma; hypothalamic diseases; Froehlich's syndrome; adenohypophysis disease; hypophysis disease; hypophysis tumor/adenoma; pituitary growth hormone; adenohypophysis hypofunction; adrenohypophysis hyperfunction; hypothalamic hypogonadism; Kallman's syndrome (anosmia, hyposmia); functional or psychogenic amenorrhea; hypopituitarism; hypothalamic hypothyroidism; hypothalamic-adrenal dysfunctions; idiopathic hyperprolactinemia; hypothalamic disorders of growth hormone deficiency; idiopathic growth hormone deficiency; dwarfism; gigantism; acromegaly; disturbed biological and circadian rhythms; and sleep disturbances associated with such diseases as neurological disorders, heart and lung diseases, mental illness, and addictions; migraine; hyperalgesia; enhanced or exaggerated sensitivity to pain, such as hyperlgesia, causalgia and allodynia; acute pain; burn pain; atypical facial pain; neuropathic pain; back pain; complex regional pain syndromes I and II; arthritic pain; sports injury pain; pain related to infection, *e.g.*, HIV, post-polio syndrome, and post-herpetic neuralgia; phantom limb pain; labour pain; cancer pain; post-chemotherapy pain; post-stroke pain; post-operative pain; neuralgia; and tolerance to narcotics or withdrawal from narcotics; sleep disorders; sleep apnea; narcolepsy; insomnia; parasomnia; jet-lag syndrome; and other neurodegenerative disorders, which includes nosological entities such as disinhibition-dementia-parkinsonism-amyotrophy complex; pallido-ponto-nigral degeneration; and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.

With the availability of complete genomic sequences for many organisms today, including *Homo sapiens*, it has become clear that there is a need for data mining techniques to extract the information in them, *e.g.*, gene prediction programs. Of these, the most successful ones are those based on the comparison of known protein or protein-derived information, or those that use expressed sequence tags (ESTs) to predict gene location and structure.

One such algorithm is GeneWise. It bases its exon prediction on the use of Hidden Markov Models (HMMs) of proteins to be compared against a genomic sequence, so that the translation of the sequence will match the model in a similar way to other HMM profile searches (Eddy, *Curr. Opin. Struct. Biol.* 6(3):361-5 (1996), and allowing the presence of long insertions as long as they include donor and acceptor site sequences at both ends.

To take advantage of the algorithm, the models for different protein families must be built so that they represent the full-length sequences instead of the most common features in them. This is a major difference with existing HMM databases such as Pfam (Sonnhammer *et al.*, *Proteins* 28(3): 405-20 (1997), in which each model is built to represent a family of proteins as broad as possible with minimum overlap between them.

In the present approach, the sequences were subdivided in several families so that the similarity inside of a group of them was over 50%. Given this approach, there are several points of overlap between different families when analyzing a sequence, so the discrimination must be done after the search is completed.

Several resources that include expert-supervised classifications are used to select the best groups of sequences, *e.g.*, the GPCR database (Horn *et al.*, *Nucleic Acids Res.* 26(1): 275-9 (1998)), PKR (Smith *et al.*, *Trends Biochem. Sci.* 22(11): 444-6 (1997)), NuclearRdb (Horn *et al.*, *Nucleic Acids Res.* 29:346-349 (2001)), IOCH (Le Novere *et al.*, *Nucleic Acids Res.* 27(1):340-2 (1999)), Enzyme (Bairoch, *Nucleic Acids Res.* 28:304-305 (2000)) and Swiss-Prot (Bairoch *et al.*, *Nucleic Acids Res.* 28:45-48 (2000)). When none is available, or the sequences included in some groups are too disrinatly related, the grouping must be done manually, using the ClustalW (Thompson *et al.*, *Nucleic Acids Res.* 22:4673-4680 (1994)) package to measure the distance between different sequences.

The present model was built from multiple sequence alignments of the different protein families obtained with DiAlign 2 (Morgenstern, *Bioinformatics* 15(3):211-8(1999)). DiAlign works based on segment-to-segment comparisons instead of arbitrary thresholds for gap opening and extension, which makes it ideally

suited for building models that represent an entire, full-length sequence, since the alignments built this way have more match states that would be assigned as insertion states when using other alignment algorithms. The models were built using the standard HMMer package.

5 To search for new genes, a genome-wide scan was done on the University of California at Santa Cruz sequences, using the GeneWise algorithm. It translates the genomic sequence on the fly to proteins and can therefore maintain a reading frame through insertions and deletions. The algorithm also rewards gaps in the genomic sequence relative to the model if they are encapsulated within introns, like splice
10 structure.

For each superfamily of proteins, a classification was obtained in which the sequences are grouped by length and similarity. Each one of these groups was then used to build a HMM profile representing this group of sequences. This approach aims to have models that can represent the full length of the encoded proteins for a
15 whole range of proteins, without being too specific for any one of them or being too general, as would be a HMM built for large groups of sequences. This classification was based either on existing expert-supervised classifications, or by retrieval of sequences and classification based on pairwise alignment distances.

These models were then searched against the October 2000 Fixed Release
20 (with its subsequent corrections) and the April 2001 Fixed Release (Tables I and II, respectively) of the Santa Cruz contigs using the Paracel GeneMatcher+ Hardware Accelerator with the GeneWise algorithm. The sequences were chopped at 100 Kb with an overlap of 1 Kb. Each one of the superfamilies required between 3 and 6 days to complete and generate results. The results represent the coding regions of
25 the complete final protein as it is found in the organism.

The cross-validation of the results was done in two steps. First, all of the hits with an E-value lower than 10^{-8} that did not overlap with one another were selected, and in the event of overlapping, the one with lowest E-value was selected. After selecting all of those matches, the DNA sequences were compared against the
30 RefSeq database (Pruitt *et al.*, *Trends Genet.* 16(1):44-47 (2000)) using BLAST (Altschul *et al.*, *Nucleic Acids Res.* 25:3389-3402 (1997)).

Over 80% of the sequences were 90% or more identical to an existing human RefSeq entry and/or mRNAs from GenBank. The differences are usually due to picking the wrong model for a certain sequence that appears as a hit more than once
35 in different families, being a different valid splice variant, which can be tested by comparing to the EST database, or by addition of a small last exon to complete the

match instead of accept an stop codon in a previous one. In all of such cases, the results are easily and quickly corrected by eye. Very rarely the algorithm will actually make a wrong prediction, which is consistent with the expected behaviour (Guigo *et al.*, *Genome Res.* 10(10):1631-42 (2000)).

5 Of the remaining sequences, over 50% have a match over 90% identical in the public domain protein databases, and the differences between those sequences in the databases and the potential translations is basically the same as the differences between the DNA sequences and the RefSeq entries.

10 The full sequences of the protein kinase genes and splice variants are shown in the sequence listing. The amino acids encoded by these nucleic acids are also set forth in the sequence listing.

A number of the genes were linked with markers known to be associated with human diseases genes. These are shown in Table IV. The diseases were linked to the HMM genes in the following manner: (1) the HMM gene models were
15 compared to the consensus of the human genome sequence, located and the results kept in a relational database; (2) all possible markers (Sequence Tagged Sites (STS's)) (public or deCODE genetics) are also located in the same consensus using ePCR or BLAT and results kept in a relational database; and (3) LOD scores for diseases are linked to markers. A span of one LOD drop around the marker was also
20 given. A computer program takes each LOD peak and links it to the consensus through the markerhit in the database. The database is then queried for all HMM genes within the span of one LOD drop or a minimum of 15 Mb in each direction from the marker. The output is the name of the peak marker and its distance to the HMM gene.

25 NUCLEIC ACIDS OF THE INVENTION

Accordingly, the invention pertains to isolated nucleic acid molecules comprising human protein kinase genes. The term, "protein kinase", as used herein, refers to an isolated nucleic acid molecule selected from the group consisting of
30 SEQ ID NOs: 1-80 (odd numbers), and also to a portion or fragment of the isolated nucleic acid molecule (*e.g.*, cDNA or the gene) that encodes protein kinase polypeptide (*e.g.*, a polypeptide selected from the group consisting of SEQ ID NOs: 1-80 (even numbers)). In a preferred embodiment, the isolated nucleic acid molecule comprises a nucleic acid molecule selected from the group consisting of
35 SEQ ID NOs: 1-80 (odd numbers) or the complement of such a nucleic acid molecule.

The isolated nucleic acid molecules of the present invention can be RNA, for example, mRNA, or DNA, such as cDNA and genomic DNA. DNA molecules can be double-stranded or single-stranded; single stranded RNA or DNA can be either the coding, or sense, strand or the non-coding, or antisense, strand. The nucleic acid molecule can include all or a portion of the coding sequence of the gene and can further comprise additional non-coding sequences such as introns and non-coding 3' and 5' sequences (including regulatory sequences, for example). Additionally, the nucleic acid molecule can be fused to a marker sequence, for example, a sequence that encodes a polypeptide to assist in isolation or purification of the polypeptide. Such sequences include, but are not limited to, those that encode a glutathione-S-transferase (GST) fusion protein and those that encode a hemagglutinin A (HA) polypeptide marker from influenza.

An "isolated" nucleic acid molecule, as used herein, is one that is separated from nucleic acids that normally flank the gene or nucleotide sequence (as in genomic sequences) and/or has been completely or partially purified from other transcribed sequences (*e.g.*, as in an RNA library). For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid molecule comprises at least about 50, 80 or 90% (on a molar basis) of all macromolecular species present. With regard to genomic DNA, the term "isolated" also can refer to nucleic acid molecules that are separated from the chromosome with which the genomic DNA is naturally associated. For example, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotides which flank the nucleic acid molecule in the genomic DNA of the cell from which the nucleic acid molecule is derived.

The nucleic acid molecule can be fused to other coding or regulatory sequences and still be considered isolated. Thus, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous host cells, as well as partially or substantially purified DNA molecules in solution. "Isolated" nucleic acid molecules also encompass *in vivo* and *in vitro* RNA

transcripts of the DNA molecules of the present invention. An isolated nucleic acid molecule or nucleotide sequence can include a nucleic acid molecule or nucleotide sequence that is synthesized chemically or by recombinant means. Therefore, recombinant DNA contained in a vector is included in the definition of “isolated” as used herein. Also, isolated nucleotide sequences include recombinant DNA molecules in heterologous organisms, as well as partially or substantially purified DNA molecules in solution. *In vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention are also encompassed by “isolated” nucleotide sequences. Such isolated nucleotide sequences are useful in the manufacture of the encoded polypeptide, as probes for isolating homologous sequences (*e.g.*, from other mammalian species), for gene mapping (*e.g.*, by *in situ* hybridization with chromosomes), or for detecting expression of the gene in tissue (*e.g.*, human tissue), such as by Northern blot analysis.

The present invention also pertains to nucleic acid molecules which are not necessarily found in nature but which encode a protein kinase polypeptide (*e.g.*, a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-80 (even numbers)), or another splicing variant of a protein kinase polypeptide or polymorphic variant thereof. Thus, for example, DNA molecules which comprise a sequence that is different from the naturally-occurring nucleotide sequence but which, due to the degeneracy of the genetic code, encode a protein kinase polypeptide of the present invention are also the subject of this invention. The invention also encompasses nucleotide sequences encoding portions (fragments), or encoding variant polypeptides such as analogues or derivatives of a protein kinase polypeptide. Such variants can be naturally-occurring, such as in the case of allelic variation or single nucleotide polymorphisms, or non-naturally-occurring, such as those induced by various mutagens and mutagenic processes. Intended variations include, but are not limited to, addition, deletion and substitution of one or more nucleotides that can result in conservative or non-conservative amino acid changes, including additions and deletions. Preferably the nucleotide (and/or resultant amino acid) changes are silent or conserved; that is, they do not alter the characteristics or activity of a protein kinase polypeptide. In one preferred embodiment, the nucleotide sequences are fragments that comprise one or more polymorphic microsatellite markers. In another preferred embodiment, the nucleotide sequences are fragments that comprise one or more single nucleotide polymorphisms in a protein kinase gene.

Other alterations of the nucleic acid molecules of the invention can include, for example, labeling, methylation, internucleotide modifications such as uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoamidates, carbamates), charged linkages (*e.g.*, phosphorothioates, phosphorodithioates), pendent moieties (*e.g.*, polypeptides), intercalators (*e.g.*, acridine, psoralen), chelators, alkylators, and modified linkages (*e.g.*, alpha anomeric nucleic acids). Also included are synthetic molecules that mimic nucleic acid molecules in the ability to bind to designated sequences via hydrogen bonding and other chemical interactions. Such molecules include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of the molecule.

The invention also pertains to nucleic acid molecules that hybridize under high stringency hybridization conditions, such as for selective hybridization, to a nucleotide sequence described herein (*e.g.*, nucleic acid molecules which specifically hybridize to a nucleotide sequence encoding polypeptides described herein, and, optionally, have an activity of the polypeptide). In one embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers). In another embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleotide sequence encoding an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-80 (even numbers) or a polymorphic variant thereof. In a preferred embodiment, the variant that hybridizes under high stringency hybridizations has an activity of a protein kinase.

Such nucleic acid molecules can be detected and/or isolated by specific hybridization (*e.g.*, under high stringency conditions). "Specific hybridization," as used herein, refers to the ability of a first nucleic acid to hybridize to a second nucleic acid in a manner such that the first nucleic acid does not hybridize to any nucleic acid other than to the second nucleic acid (*e.g.*, when the first nucleic acid has a higher similarity to the second nucleic acid than to any other nucleic acid in a sample wherein the hybridization is to be performed). "Stringency conditions" for hybridization is a term of art which refers to the incubation and wash conditions, *e.g.*, conditions of temperature and buffer concentration, which permit hybridization of a particular nucleic acid to a second nucleic acid; the first nucleic acid may be perfectly (*i.e.*, 100%) complementary to the second, or the first and second may share some degree of complementarity which is less than perfect (*e.g.*, 70%, 75%,

85%, 90%, 95%). For example, certain high stringency conditions can be used which distinguish perfectly complementary nucleic acids from those of less complementarity. "High stringency conditions", "moderate stringency conditions" and "low stringency conditions" for nucleic acid hybridizations are explained on
5 pages 2.10.1-2.10.16 and pages 6.3.1-6.3.6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. *et al.*, "Current Protocols in Molecular Biology", John Wiley & Sons, (1998), the entire teachings of which are incorporated by reference herein). The exact conditions which determine the stringency of hybridization depend not only on ionic strength (*e.g.*, 0.2X SSC, 0.1X SSC), temperature (*e.g.*,
10 room temperature, 42°C, 68°C) and the concentration of destabilizing agents such as formamide or denaturing agents such as SDS, but also on factors such as the length of the nucleic acid sequence, base composition, percent mismatch between hybridizing sequences and the frequency of occurrence of subsets of that sequence within other non-identical sequences. Thus, equivalent conditions can be
15 determined by varying one or more of these parameters while maintaining a similar degree of identity or similarity between the two nucleic acid molecules. Typically, conditions are used such that sequences at least about 60%, at least about 70%, at least about 80%, at least about 90% or at least about 95% or more identical to each other remain hybridized to one another. By varying hybridization conditions from a
20 level of stringency at which no hybridization occurs to a level at which hybridization is first observed, conditions which will allow a given sequence to hybridize (*e.g.*, selectively) with the most similar sequences in the sample can be determined.

Exemplary conditions are described in Krause, M.H. and S.A. Aaronson, *Methods in Enzymology* 200:546-556 (1991), and in, Ausubel, *et al.*, "Current
25 *Protocols in Molecular Biology*", John Wiley & Sons, (1998), which describes the determination of washing conditions for moderate or low stringency conditions. Washing is the step in which conditions are usually set so as to determine a minimum level of complementarity of the hybrids. Generally, starting from the lowest temperature at which only homologous hybridization occurs, each °C by
30 which the final wash temperature is reduced (holding SSC concentration constant) allows an increase by 1% in the maximum extent of mismatching among the sequences that hybridize. Generally, doubling the concentration of SSC results in an increase in T_m of $\approx 17^\circ\text{C}$. Using these guidelines, the washing temperature can be determined empirically for high, moderate or low stringency, depending on the level
35 of mismatch sought.

For example, a low stringency wash can comprise washing in a solution containing 0.2X SSC/0.1% SDS for 10 minutes at room temperature; a moderate stringency wash can comprise washing in a prewarmed solution (42°C) solution containing 0.2X SSC/0.1% SDS for 15 minutes at 42°C; and a high stringency wash can comprise washing in prewarmed (68°C) solution containing 0.1X SSC/0.1% SDS for 15 minutes at 68°C. Furthermore, washes can be performed repeatedly or sequentially to obtain a desired result as known in the art. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleic acid molecule and the primer or probe used.

The percent identity of two nucleotide or amino acid sequences can be determined by aligning the sequences for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first sequence). The nucleotides or amino acids at corresponding positions are then compared, and the percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions x 100). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 60%, and even more preferably at least 70%, 80%, 90% or 95% of the length of the reference sequence. The actual comparison of the two sequences can be accomplished by well-known methods, for example, using a mathematical algorithm. A preferred, non-limiting example of such a mathematical algorithm is described in Karlin *et al.*, *Proc. Natl. Acad. Sci. USA* 90:5873-5877 (1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) as described in Altschul *et al.*, *Nucleic Acids Res.* 25:389-3402 (1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, NBLAST) can be used. In one embodiment, parameters for sequence comparison can be set at score=100, wordlength=12, or can be varied (*e.g.*, W=5 or W=20).

Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, *CABIOS* 4(1):11-17 (1988). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package (Accelrys, Cambridge, UK). When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art and include ADVANCE and ADAM as described in Torellis and

Robotti, *Comput. Appl. Biosci.* 10:3-5 (1994); and FASTA described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-8 (1988).

In another embodiment, the percent identity between two amino acid sequences can be accomplished using the GAP program in the GCG software using
5 either a BLOSUM63 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. In yet another embodiment, the percent identity between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using a gap weight of 50 and a length weight of 3.

10 The present invention also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), or the complement of such a sequence, and also provides isolated nucleic acid molecules that contain a fragment
15 or portion that hybridizes under highly stringent conditions to a nucleotide sequence encoding an amino acid sequence selected SEQ ID NOs: 1-80 (even numbers), or polymorphic variant thereof. The nucleic acid fragments of the invention are at least about 15, preferably at least about 18, 20, 23 or 25 nucleotides, and can be 30, 40, 50, 100, 200 or more nucleotides in length. Longer fragments, for example, 30 or
20 more nucleotides in length, which encode antigenic polypeptides described herein are particularly useful, such as for the generation of antibodies as described below.

In a related aspect, the nucleic acid fragments of the invention are used as probes or primers in assays such as those described herein. "Probes" or "primers" are oligonucleotides that hybridize in a base-specific manner to a complementary
25 strand of nucleic acid molecules. Such probes and primers include polypeptide nucleic acids, as described in Nielsen *et al.*, *Science* 254:1497-1500 (1991).

Typically, a probe or primer comprises a region of nucleotide sequence that hybridizes to at least about 15, typically about 20-25, and more typically about 40, 50 or 75, consecutive nucleotides of a nucleic acid molecule comprising a
30 contiguous nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), or the complement of such a sequence, or a sequence encoding an amino acid sequence selected from SEQ ID NOs: 1-80 (even numbers), or polymorphic variant thereof. In preferred embodiments, a probe or primer comprises 100 or fewer nucleotides, preferably from 6 to 50 nucleotides, preferably
35 from 12 to 30 nucleotides. In other embodiments, the probe or primer is at least 70% identical to the contiguous nucleotide sequence or to the complement of the

contiguous nucleotide sequence, preferably at least 80% identical, more preferably at least 90% identical, even more preferably at least 95% identical, or even capable of selectively hybridizing to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. Often, the probe or primer further comprises a label, *e.g.*, radioisotope, fluorescent compound, enzyme, or enzyme co-factor.

The nucleic acid molecules of the invention such as those described above can be identified and isolated using standard molecular biology techniques and the sequence information provided herein. For example, nucleic acid molecules can be amplified and isolated by the polymerase chain reaction using synthetic oligonucleotide primers designed based on one or more of the sequences selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), or the complement of such a sequence, or designed based on nucleotides based on sequences encoding one or more of the amino acid sequences provided herein. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (Eds. Innis *et al.*, Academic Press, San Diego, CA, 1990); Mattila *et al.*, *Nucl. Acids Res.* 19:4967 (1991); Eckert *et al.*, *PCR Methods and Applications* 1:17 (1991); PCR (eds. McPherson *et al.*, IRL Press, Oxford); and U.S. Patent 4,683,202. The nucleic acid molecules can be amplified using cDNA, mRNA or genomic DNA as a template, cloned into an appropriate vector and characterized by DNA sequence analysis.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4:560 (1989), Landegren *et al.*, *Science* 241:1077 (1988), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

The amplified DNA can be radiolabelled and used as a probe for screening a cDNA library derived from human cells, mRNA in zap express, ZIPLOX or other suitable vector. Corresponding clones can be isolated, DNA can obtained following *in vivo* excision, and the cloned insert can be sequenced in either or both orientations by art recognized methods to identify the correct reading frame encoding a

polypeptide of the appropriate molecular weight. For example, the direct analysis of the nucleotide sequence of nucleic acid molecules of the present invention can be accomplished using well-known methods that are commercially available. See, for example, Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind *et al.*, *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)). Using these or similar methods, the polypeptide and the DNA encoding the polypeptide can be isolated, sequenced and further characterized.

Antisense nucleic acid molecules of the invention can be designed using the nucleotide sequences of one or more of SEQ ID NOs: 1-80 (odd numbers) and/or the complement of one or more of SEQ ID NOs: 1-80 (odd numbers), and/or a portion of one or more of SEQ ID NOs: 1-80 (odd numbers), or the complement of one or more of SEQ ID NOs: 1-80 (odd numbers) and/or a sequence encoding the amino acid sequences of one or more of SEQ ID NOs: 1-80 (even numbers), or encoding a portion of one or more of SEQ ID NOs: 1-80 (even numbers), and constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid molecule (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Alternatively, the antisense nucleic acid molecule can be produced biologically using an expression vector into which a nucleic acid molecule has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid molecule will be of an antisense orientation to a target nucleic acid of interest).

In general, the isolated nucleic acid sequences of the invention can be used as molecular weight markers on Southern gels, and as chromosome markers that are labeled to map related gene positions. The nucleic acid sequences can also be used to compare with endogenous DNA sequences in patients to identify one or more of the disorders described above, and as probes, such as to hybridize and discover related DNA sequences or to subtract out known sequences from a sample. The nucleic acid sequences can further be used to derive primers for genetic fingerprinting, to raise anti-polypeptide antibodies using DNA immunization techniques, and as an antigen to raise anti-DNA antibodies or elicit immune responses. Portions or fragments of the nucleotide sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as

polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Additionally, the nucleotide sequences of the invention can be used to identify and express recombinant polypeptides for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding polypeptide is expressed, either constitutively, during tissue differentiation, or in diseased states. The nucleic acid sequences can additionally be used as reagents in the screening and/or diagnostic assays described herein, and can also be included as components of kits (*e.g.*, reagent kits) for use in the screening and/or diagnostic assays described herein.

Another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers) and the complements thereof (or a portion thereof). Yet another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule encoding an amino acid sequence of SEQ ID NOs: 1-80 (even numbers) or polymorphic variant thereof. The constructs comprise a vector (*e.g.*, an expression vector) into which a sequence of the invention has been inserted in a sense or antisense orientation. As used herein, the term “vector” refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a “plasmid”, which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors, expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses) that serve equivalent functions.

Preferred recombinant expression vectors of the invention comprise a nucleic acid molecule of the invention in a form suitable for expression of the nucleic acid

molecule in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, “operably linked” or
5 “operatively linked” is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term “regulatory
10 sequence” is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, “Gene Expression Technology”, *Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain
15 host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed and the level of expression of polypeptide desired. The expression vectors of the invention can be introduced into host cells to thereby produce polypeptides, including fusion polypeptides, encoded
20 by nucleic acid molecules as described herein.

The recombinant expression vectors of the invention can be designed for expression of a polypeptide of the invention in prokaryotic or eukaryotic cells, *e.g.*, bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors), yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel,
25 *supra*. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms “host cell” and
30 “recombinant host cell” are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of
35 the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, a nucleic acid molecule of the invention can be expressed in bacterial cells (*e.g.*, *E. coli*), insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

5 Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms “transformation” and “transfection” are intended to refer to a variety of art-recognized techniques for introducing a foreign nucleic acid molecule (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, 10 DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells 15 may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid molecules encoding a selectable 20 marker can be introduced into a host cell on the same vector as the nucleic acid molecule of the invention or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid molecule can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

25 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) a polypeptide of the invention. Accordingly, the invention further provides methods for producing a polypeptide using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector 30 encoding a polypeptide of the invention has been introduced) in a suitable medium such that the polypeptide is produced. In another embodiment, the method further comprises isolating the polypeptide from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is 35 a fertilized oocyte or an embryonic stem cell into which a nucleic acid molecule of the invention has been introduced (*e.g.*, an exogenous protein kinase gene, or an

exogenous nucleic acid encoding a protein kinase polypeptide). Such host cells can then be used to create non-human transgenic animals in which exogenous nucleotide sequences have been introduced into the genome or homologous recombinant animals in which endogenous nucleotide sequences have been altered. Such animals are useful for studying the function and/or activity of the nucleotide sequence and polypeptide encoded by the sequence and for identifying and/or evaluating modulators of their activity. As used herein, a “transgenic animal” is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal include a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens and amphibians. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an “homologous recombinant animal” is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Pat. No. 4,873,191 and in Hogan, *Manipulating the Mouse Embryo* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, *Current Opinion in BioTechnology* 2:823-829 (1991) and in PCT Publication Nos. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169. Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.*, *Nature* 385:810-813 (1997) and PCT Publication Nos. WO 97/07668 and WO 97/07669.

POLYPEPTIDES OF THE INVENTION

The present invention also pertains to isolated polypeptides encoded by protein kinases (“protein kinase polypeptides”) and fragments and variants thereof, as well as polypeptides encoded by nucleotide sequences described herein (*e.g.*,

other splicing variants). The term “polypeptide” refers to a polymer of amino acids, and not to a specific length; thus, peptides, oligopeptides and proteins are included within the definition of a polypeptide. As used herein, a polypeptide is said to be “isolated” or “purified” when it is substantially free of cellular material when it is isolated from recombinant and non-recombinant cells, or free of chemical precursors or other chemicals when it is chemically synthesized. A polypeptide, however, can be joined to another polypeptide with which it is not normally associated in a cell (*e.g.*, in a “fusion protein”) and still be “isolated” or “purified.”

The polypeptides of the invention can be purified to homogeneity. It is understood, however, that preparations in which the polypeptide is not purified to homogeneity are useful. The critical feature is that the preparation allows for the desired function of the polypeptide, even in the presence of considerable amounts of other components. Thus, the invention encompasses various degrees of purity. In one embodiment, the language “substantially free of cellular material” includes preparations of the polypeptide having less than about 30% (by dry weight) other proteins (*i.e.*, contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins.

When a polypeptide is recombinantly produced, it can also be substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, less than about 10%, or less than about 5% of the volume of the polypeptide preparation. The language “substantially free of chemical precursors or other chemicals” includes preparations of the polypeptide in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment, the language “substantially free of chemical precursors or other chemicals” includes preparations of the polypeptide having less than about 30% (by dry weight) chemical precursors or other chemicals, less than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals.

In one embodiment, a polypeptide of the invention comprises an amino acid sequence encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), or the complement of such a nucleic acid, or portions thereof, *e.g.*, SEQ ID NO:1-80 (odd numbers), or a portion or polymorphic variant thereof. However, the polypeptides of the invention also encompass fragment and sequence variants. Variants include a substantially homologous polypeptide encoded by the same genetic locus in an organism, *i.e.*, an allelic variant, as well as other splicing variants. Variants also

encompass polypeptides derived from other genetic loci in an organism, but having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-80 (odd numbers), or a complement of such a sequence, or portions thereof, or having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of nucleotide sequences encoding SEQ ID NOs: 1-80 (odd numbers), or polymorphic variants thereof. Variants also include polypeptides substantially homologous or identical to these polypeptides but derived from another organism, *i.e.*, an ortholog. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by chemical synthesis. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by recombinant methods.

As used herein, two polypeptides (or a region of the polypeptides) are substantially homologous or identical when the amino acid sequences are at least about 45-55%, typically at least about 70-75%, more typically at least about 80-85%, and most typically greater than about 90% or 95% or more homologous or identical. A substantially homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid molecule hybridizing to one or more of SEQ ID NOs: 1-80 (odd numbers), or portion thereof, under stringent conditions as more particularly described above, or will be encoded by a nucleic acid molecule hybridizing to a nucleic acid sequence encoding one of SEQ ID NOs: 1-80 (odd numbers), a portion thereof or polymorphic variant thereof, under stringent conditions as more particularly described thereof.

To determine the percent homology or identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one polypeptide or nucleic acid molecule for optimal alignment with the other polypeptide or nucleic acid molecule). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence, then the molecules are homologous at that position. As used herein, amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity". The percent homology between the two sequences is a function of the number of identical positions shared by the sequences

(i.e., percent homology equals the number of identical positions/total number of positions times 100).

The invention also encompasses polypeptides having a lower degree of identity but having sufficient similarity so as to perform one or more of the same functions performed by a polypeptide encoded by a nucleic acid molecule of the invention. Similarity is determined by conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Conservative substitutions are likely to be phenotypically silent. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al.*, *Science* 247:1306-1310 (1990).

A variant polypeptide can differ in amino acid sequence by one or more substitutions, deletions, insertions, inversions, fusions, and truncations or a combination of any of these. Further, variant polypeptides can be fully functional or can lack function in one or more activities. Fully functional variants typically contain only conservative variation or variation in non-critical residues or in non-critical regions. Functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree. Non-functional variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution, insertion, inversion, or deletion in a critical residue or critical region.

Amino acids that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.*, *Science* 244:1081-1085 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity *in vitro*, or *in vitro* proliferative activity. Sites that are critical for polypeptide activity can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol.* 224:899-904 (1992); de Vos *et al.*, *Science* 255:306-312 (1992)).

The invention also includes polypeptide fragments of the polypeptides of the invention. Fragments can be derived from a polypeptide encoded by a nucleic acid molecule comprising one of SEQ ID NOs: 1-80 (odd numbers), or a complement of such a nucleic acid (*e.g.*, SEQ ID NOs: 1-80 (odd numbers), or other variants).

However, the invention also encompasses fragments of the variants of the polypeptides described herein. As used herein, a fragment comprises at least 6 contiguous amino acids. Useful fragments include those that retain one or more of the biological activities of the polypeptide as well as fragments that can be used as an immunogen to generate polypeptide-specific antibodies.

Biologically active fragments (peptides which are, for example, 6, 9, 12, 15, 16, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) can comprise a domain, segment, or motif that has been identified by analysis of the polypeptide sequence using well-known methods, *e.g.*, signal peptides, extracellular domains, one or more transmembrane segments or loops, ligand binding regions, zinc finger domains, DNA binding domains, acylation sites, glycosylation sites, or phosphorylation sites.

Fragments can be discrete (not fused to other amino acids or polypeptides) or can be within a larger polypeptide. Further, several fragments can be comprised within a single larger polypeptide. In one embodiment a fragment designed for expression in a host can have heterologous pre- and pro-polypeptide regions fused to the amino terminus of the polypeptide fragment and an additional region fused to the carboxyl terminus of the fragment.

The invention thus provides chimeric or fusion polypeptides. These comprise a polypeptide of the invention operatively linked to a heterologous protein or polypeptide having an amino acid sequence not substantially homologous to the polypeptide. "Operatively linked" indicates that the polypeptide and the heterologous protein are fused in-frame. The heterologous protein can be fused to the N-terminus or C-terminus of the polypeptide. In one embodiment the fusion polypeptide does not affect function of the polypeptide *per se*. For example, the fusion polypeptide can be a GST-fusion polypeptide in which the polypeptide sequences are fused to the C-terminus of the GST sequences. Other types of fusion polypeptides include, but are not limited to, enzymatic fusion polypeptides, for example beta-galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions and Ig fusions. Such fusion polypeptides, particularly poly-His fusions, can facilitate the purification of recombinant polypeptide. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of a polypeptide can be

increased using a heterologous signal sequence. Therefore, in another embodiment, the fusion polypeptide contains a heterologous signal sequence at its N-terminus.

EP-A-O 464 533 discloses fusion proteins comprising various portions of immunoglobulin constant regions. The Fc is useful in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). In drug discovery, for example, human proteins have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists. Bennett *et al.*, *Journal of Molecular Recognition*, 8:52-58 (1995) and Johanson *et al.*, *The Journal of Biological Chemistry*, 270,16:9459-9471 (1995). Thus, this invention also encompasses soluble fusion polypeptides containing a polypeptide of the invention and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE).

A chimeric or fusion polypeptide can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of nucleic acid fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive nucleic acid fragments which can subsequently be annealed and re-amplified to generate a chimeric nucleic acid sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST protein). A nucleic acid molecule encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide.

The isolated polypeptide can be purified from cells that naturally express it, purified from cells that have been altered to express it (recombinant), or synthesized using known protein synthesis methods. In one embodiment, the polypeptide is produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the polypeptide is cloned into an expression vector, the expression vector introduced into a host cell and the polypeptide expressed in the host cell. The polypeptide can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques.

In general, polypeptides of the present invention can be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns using art-recognized methods. The polypeptides of the present invention can be

used to raise antibodies or to elicit an immune response. The polypeptides can also be used as a reagent, *e.g.*, a labeled reagent, in assays to quantitatively determine levels of the polypeptide or a molecule to which it binds (*e.g.*, a ligand) in biological fluids. The polypeptides can also be used as markers for cells or tissues in which the corresponding polypeptide is preferentially expressed, either constitutively, during tissue differentiation, or in a diseased state. The polypeptides can be used to isolate a corresponding binding agent, *e.g.*, ligand, such as, for example, in an interaction trap assay, and to screen for peptide or small molecule antagonists or agonists of the binding interaction.

ANTIBODIES OF THE INVENTION

Polyclonal and/or monoclonal antibodies that specifically bind one form of the gene product but not to the other form of the gene product are also provided. Antibodies that bind a portion of either the variant or the reference gene product that contains the polymorphic site or sites are also provided. The invention provides antibodies to the polypeptides and polypeptide fragments of the invention, *e.g.*, having an amino acid sequence of one of SEQ ID NOs: 1-80 (even numbers) or a portion thereof, or having an amino acid sequence encoded by a nucleic acid molecule comprising all or a portion of SEQ ID NOs: 1-80 (odd numbers), or a complement or another variant or portion thereof. The term “antibody” as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds an antigen. A molecule that specifically binds to a polypeptide of the invention is a molecule that binds to that polypeptide or a fragment thereof, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the polypeptide. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and F(ab')₂ fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies that bind to a polypeptide of the invention. The term “monoclonal antibody” or “monoclonal antibody composition”, as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide of the invention. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polypeptide of the invention with which it immunoreacts.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a desired immunogen, *e.g.*, polypeptide of the invention or fragment thereof. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules directed against the polypeptide can be isolated from the mammal (*e.g.*, from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. At an appropriate time after immunization, *e.g.*, when the antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein, *Nature* 256:495-497 (1975), the human B cell hybridoma technique (Kozbor *et al.*, *Immunol. Today* 4:72 (1983)), the EBV-hybridoma technique (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, 1985, Inc., pp. 77-96) or trioma technique. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* (1994) Coligan *et al.* (eds.) John Wiley & Sons, Inc., New York, NY). Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes) from a mammal immunized with an immunogen as described above, and the culture supernatants of the resulting hybridoma cells are screened to identify a hybridoma producing a monoclonal antibody that binds a polypeptide of the invention.

Any of the many well known protocols used for fusing lymphocytes and immortalized cell lines can be applied for the purpose of generating a monoclonal antibody to a polypeptide of the invention (see, *e.g.*, *Current Protocols in Immunology*, *supra*; Galfre *et al.*, *Nature* 266:55052 (1977); R.H. Kenneth, in *Monoclonal Antibodies: A New Dimension In Biological Analyses*, Plenum Publishing Corp., New York, New York (1980); and Lerner, *Yale J. Biol. Med.* 54:387-402 (1981). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods that also would be useful.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody to a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (*e.g.*, an antibody phage display library) with the polypeptide to thereby isolate immunoglobulin library members that bind the polypeptide. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *SurfZAP*TM

Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.*, *Bio/Technology* 9:1370-1372 (1991); Hay *et al.*, *Hum. Antibod. Hybridomas* 3:81-85 (1992); Huse *et al.*, *Science* 246:1275-1281 (1989); Griffiths *et al.*, *EMBO J.* 12:725-734 (1993).

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art.

In general, antibodies of the invention (*e.g.*, a monoclonal antibody) can be used to isolate a polypeptide of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. A polypeptide-specific antibody can facilitate the purification of natural polypeptide from cells and of recombinantly produced polypeptide expressed in host cells. Moreover, an antibody specific for a polypeptide of the invention can be used to detect the polypeptide (*e.g.*, in a cellular lysate, cell supernatant, or tissue sample) in order to evaluate the abundance and pattern of expression of the polypeptide. Antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection of the antibody can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, bata-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ¹²⁵I, ¹³¹I, ³⁵S or ³H.

DIAGNOSTIC AND SCREENING ASSAYS OF THE INVENTION

The present invention also pertains to a method of diagnosing or aiding in the diagnosis of a disease or condition associated with a protein kinase gene or gene product in an individual. Diagnostic assays can be designed for assessing protein kinase gene expression, or for assessing activity of protein kinase polypeptides of the invention. In one embodiment, the assays are used in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or condition associated with a protein kinase, or a defect in a protein kinase. The invention also provides for prognostic (or predictive) assays for determining whether an individual is susceptible to a disease or condition associated with a protein kinase. For example, mutations in the gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of symptoms associated with a susceptibility to a disease or condition associated with a protein kinase. Another aspect of the invention pertains to assays for monitoring the influence of agents (*e.g.*, drugs, compounds or other agents) on the gene expression or activity of polypeptides of the invention, as well as to assays for identifying agents that bind to a polypeptides. These and other assays and agents are described in further detail in the following sections.

DIAGNOSTIC ASSAYS

The nucleic acids, probes, primers, polypeptides and antibodies described herein can be used in methods of diagnosis of a susceptibility to a disease or condition associated with a protein kinase, as well as in kits useful for diagnosis of a susceptibility to a disease or condition associated with a protein kinase.

In one embodiment of the invention, susceptibility to a disease or condition associated with a protein kinase is diagnosed by detecting a polymorphism in a protein kinase as described herein. The polymorphism can be a mutation in a protein kinase, such as the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift mutation; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding

sequence of the gene; duplication of all or a part of the gene; transposition of all or a part of the gene; or rearrangement of all or a part of the gene. More than one such mutation may be present in a single gene. Such sequence changes cause a mutation in the polypeptide encoded by a protein kinase gene. For example, if the mutation is a frame shift mutation, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with a susceptibility to a disease or condition associated with a protein kinase can be a synonymous mutation in one or more nucleotides (*i.e.*, a mutation that does not result in a change in the polypeptide encoded by a protein kinase gene). Such a polymorphism may alter splicing sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of the gene. A protein kinase gene that has any of the mutations described above is referred to herein as a “mutant gene.”

In a first method of diagnosing a susceptibility to a disease or condition associated with a protein kinase, hybridization methods, such as Southern analysis, Northern analysis, or *in situ* hybridizations, can be used (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, including all supplements through 1999). For example, a biological sample from a test subject (a “test sample”) of genomic DNA, RNA, or cDNA, is obtained from an individual suspected of having, being susceptible to or predisposed for, or carrying a defect for, a susceptibility to a disease or condition associated with a protein kinase (the “test individual”). The individual can be an adult, child, or fetus. The test sample can be from any source which contains genomic DNA, such as a blood sample, sample of amniotic fluid, sample of cerebrospinal fluid, or tissue sample from skin, muscle, buccal or conjunctival mucosa, placenta, gastrointestinal tract or other organs. A test sample of DNA from fetal cells or tissue can be obtained by appropriate methods, such as by amniocentesis or chorionic villus sampling. The DNA, RNA, or cDNA sample is then examined to determine whether a polymorphism in a protein kinase is present, and/or to determine which splicing variant(s) encoded by the protein kinase is present. The presence of the polymorphism or splicing variant(s) can be indicated by hybridization of the gene in the genomic DNA, RNA, or cDNA to a nucleic acid probe. A “nucleic acid probe”, as used herein, can be a DNA probe or an RNA probe; the nucleic acid probe can contain at least one polymorphism in a protein kinase or contains a nucleic acid encoding a particular splicing variant of a protein kinase. The probe can be any of

the nucleic acid molecules described above (*e.g.*, the gene, a fragment, a vector comprising the gene, a probe or primer, etc.).

To diagnose susceptibility to a disease or condition associated with a protein kinase, the test sample containing a protein kinase is contacted with at least one nucleic acid probe to form the hybridization sample. A preferred probe for detecting mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to mRNA or genomic DNA sequences described herein. The nucleic acid probe can be, for example, a full-length nucleic acid molecule, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to appropriate mRNA or genomic DNA. For example, the nucleic acid probe can be all or a portion of one of SEQ ID NOs: 1-80 (odd numbers), or the complement thereof, or a portion thereof; or can be a nucleic acid encoding a portion of one of SEQ ID NOs: 1-80 (odd numbers). Other suitable probes for use in the diagnostic assays of the invention are described above (see *e.g.*, probes and primers discussed under the heading, "Nucleic Acids of the Invention").

The hybridization sample is maintained under conditions that are sufficient to allow specific hybridization of the nucleic acid probe to a protein kinase. "Specific hybridization", as used herein, indicates exact hybridization (*e.g.*, with no mismatches). Specific hybridization can be performed under high stringency conditions or moderate stringency conditions, for example, as described above. In a particularly preferred embodiment, the hybridization conditions for specific hybridization are high stringency.

Specific hybridization, if present, is then detected using standard methods. If specific hybridization occurs between the nucleic acid probe and the protein kinase in the test sample, then the protein kinase has the polymorphism, or is the splicing variant, that is present in the nucleic acid probe. More than one nucleic acid probe can also be used concurrently in this method. Specific hybridization of any one of the nucleic acid probes is indicative of a polymorphism in the protein kinase, or of the presence of a particular splicing variant encoding the protein kinase and is therefore diagnostic for a susceptibility to a disease or condition associated with a protein kinase.

In Northern analysis (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, *supra*) the hybridization methods described above are used to identify the presence of a polymorphism or a particular splicing variant, associated with a susceptibility to a disease or condition

associated with a protein kinase. For Northern analysis, a test sample of RNA is obtained from the individual by appropriate means. Specific hybridization of a nucleic acid probe, as described above, to RNA from the individual is indicative of a polymorphism in a protein kinase, or of the presence of a particular splicing variant encoded by a protein kinase, and is therefore diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a protein kinase.

For representative examples of use of nucleic acid probes, see, for example, U.S. Patents No. 5,288,611 and 4,851,330.

Alternatively, a peptide nucleic acid (PNA) probe can be used instead of a nucleic acid probe in the hybridization methods described above. PNA is a DNA mimic having a peptide-like, inorganic backbone, such as N-(2-aminoethyl)glycine units, with an organic base (A, G, C, T or U) attached to the glycine nitrogen via a methylene carbonyl linker (see, for example, Nielsen, P.E. *et al.*, *Bioconjugate Chemistry* 5, American Chemical Society, p. 1 (1994)). The PNA probe can be designed to specifically hybridize to a gene having a polymorphism associated with a susceptibility to a susceptibility to a disease or condition associated with a protein kinase. Hybridization of the PNA probe to a protein kinase is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a protein kinase.

In another method of the invention, mutation analysis by restriction digestion can be used to detect a mutant gene, or genes containing a polymorphism(s), if the mutation or polymorphism in the gene results in the creation or elimination of a restriction site. A test sample containing genomic DNA is obtained from the individual. Polymerase chain reaction (PCR) can be used to amplify a protein kinase (and, if necessary, the flanking sequences) in the test sample of genomic DNA from the test individual. RFLP analysis is conducted as described (see *Current Protocols in Molecular Biology*, *supra*). The digestion pattern of the relevant DNA fragment indicates the presence or absence of the mutation or polymorphism in the protein kinase, and therefore indicates the presence or absence of this susceptibility to a susceptibility to a disease or condition associated with a protein kinase.

Sequence analysis can also be used to detect specific polymorphisms in a protein kinase. A test sample of DNA or RNA is obtained from the test individual. PCR or other appropriate methods can be used to amplify the gene, and/or its flanking sequences, if desired. The sequence of a protein kinase, or a fragment of the gene, or cDNA, or fragment of the cDNA, or mRNA, or fragment of the mRNA,

is determined, using standard methods. The sequence of the gene, gene fragment, cDNA, cDNA fragment, mRNA, or mRNA fragment is compared with the known nucleic acid sequence of the gene, cDNA (*e.g.*, one or more of SEQ ID NOs: 1-80 (odd numbers), or a complement thereof, or a nucleic acid sequence encoding one of
5 SEQ ID NOs: 1-80 (odd numbers) or a fragment thereof) or mRNA, as appropriate. The presence of a polymorphism in the protein kinase indicates that the individual has a susceptibility to a susceptibility to a disease or condition associated with a protein kinase.

Allele-specific oligonucleotides can also be used to detect the presence of a
10 polymorphism in a protein kinase, through the use of dot-blot hybridization of amplified oligonucleotides with allele-specific oligonucleotide (ASO) probes (see, for example, Saiki, R. *et al.*, *Nature* 324:163-166 (1986)). An "allele-specific oligonucleotide" (also referred to herein as an "allele-specific oligonucleotide probe") is an oligonucleotide of approximately 10-50 base pairs, preferably
15 approximately 15-30 base pairs, that specifically hybridizes to a protein kinase, and that contains a polymorphism associated with a susceptibility to a susceptibility to a disease or condition associated with a protein kinase. An allele-specific oligonucleotide probe that is specific for particular polymorphisms in a protein kinase can be prepared, using standard methods (see *Current Protocols in Molecular Biology, supra*). To identify polymorphisms in the gene that are associated with a
20 susceptibility to a susceptibility to a disease or condition associated with a protein kinase, a test sample of DNA is obtained from the individual. PCR can be used to amplify all or a fragment of a protein kinase, and its flanking sequences. The DNA containing the amplified protein kinase (or fragment of the gene) is dot-blotted,
25 using standard methods (see *Current Protocols in Molecular Biology, supra*), and the blot is contacted with the oligonucleotide probe. The presence of specific hybridization of the probe to the amplified protein kinase is then detected. Specific hybridization of an allele-specific oligonucleotide probe to DNA from the individual is indicative of a polymorphism in the protein kinase, and is therefore indicative of a
30 susceptibility to a susceptibility to a disease or condition associated with a protein kinase.

In another embodiment, arrays of oligonucleotide probes that are complementary to target nucleic acid sequence segments from an individual, can be used to identify polymorphisms in a protein kinase. For example, in one
35 embodiment, an oligonucleotide array can be used. Oligonucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface

of a substrate in different known locations. These oligonucleotide arrays, also described as "Genechips™," have been generally described in the art, for example, U.S. Pat. No. 5,143,854 and PCT patent publication Nos. WO 90/15070 and 92/10092. These arrays can generally be produced using mechanical synthesis methods or light directed synthesis methods which incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis methods. See Fodor *et al.*, *Science* 251:767-777 (1991), Pirrung *et al.*, U.S. Pat. No. 5,143,854 (see also PCT Application No. WO 90/15070) and Fodor *et al.*, PCT Publication No. WO 92/10092 and U.S. Pat. No. 5,424,186, the entire teachings of each of which are incorporated by reference herein. Techniques for the synthesis of these arrays using mechanical synthesis methods are described in, *e.g.*, U.S. Pat. Nos. 5,384,261; the entire teachings of which are incorporated by reference herein.

Once an oligonucleotide array is prepared, a nucleic acid of interest is hybridized with the array and scanned for polymorphisms. Hybridization and scanning are generally carried out by methods described herein and also in, *e.g.*, published PCT Application Nos. WO 92/10092 and WO 95/11995, and U.S. Pat. No. 5,424,186, the entire teachings of which are incorporated by reference herein. In brief, a target nucleic acid sequence that includes one or more previously identified polymorphic markers is amplified by well known amplification techniques, *e.g.*, PCR. Typically, this involves the use of primer sequences that are complementary to the two strands of the target sequence both upstream and downstream from the polymorphism. Asymmetric PCR techniques may also be used. Amplified target, generally incorporating a label, is then hybridized with the array under appropriate conditions. Upon completion of hybridization and washing of the array, the array is scanned to determine the position on the array to which the target sequence hybridizes. The hybridization data obtained from the scan is typically in the form of fluorescence intensities as a function of location on the array.

Although primarily described in terms of a single detection block, *e.g.*, for detection of a single polymorphism, arrays can include multiple detection blocks, and thus be capable of analyzing multiple, specific polymorphisms. In alternate arrangements, it will generally be understood that detection blocks may be grouped within a single array or in multiple, separate arrays so that varying, optimal conditions may be used during the hybridization of the target to the array. For example, it may often be desirable to provide for the detection of those polymorphisms that fall within G-C rich stretches of a genomic sequence, separately

from those falling in A-T rich segments. This allows for the separate optimization of hybridization conditions for each situation.

Additional description of use of oligonucleotide arrays for detection of polymorphisms can be found, for example, in U.S. Patents 5,858,659 and 5,837,832, the entire teachings of which are incorporated by reference herein.

Other methods of nucleic acid analysis can be used to detect polymorphisms in a protein kinase or variants encoding by a protein kinase. Representative methods include direct manual sequencing (Church and Gilbert, *Proc. Natl. Acad. Sci. USA* 81:1991-1995 (1988); Sanger, F. *et al.*, *Proc. Natl. Acad. Sci. USA* 74:5463-5467 (1977); Beavis *et al.* U.S. Pat. No. 5,288,644); automated fluorescent sequencing; single-stranded conformation polymorphism assays (SSCP); clamped denaturing gel electrophoresis (CDGE); denaturing gradient gel electrophoresis (DGGE) (Sheffield, V.C. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:232-236 (1989)), mobility shift analysis (Orita, M. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:2766-2770 (1989)), restriction enzyme analysis (Flavell *et al.*, *Cell* 15:25 (1978); Geever, *et al.*, *Proc. Natl. Acad. Sci. USA* 78:5081 (1981)); heteroduplex analysis; chemical mismatch cleavage (CMC) (Cotton *et al.*, *Proc. Natl. Acad. Sci. USA* 85:4397-4401 (1985)); RNase protection assays (Myers, R.M. *et al.*, *Science* 230:1242 (1985)); use of polypeptides which recognize nucleotide mismatches, such as *E. coli* mutS protein; allele-specific PCR, for example.

In another embodiment of the invention, diagnosis of a susceptibility to a susceptibility to a disease or condition associated with a protein kinase can also be made by examining expression and/or composition of a protein kinase polypeptide, by a variety of methods, including enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. A test sample from an individual is assessed for the presence of an alteration in the expression and/or an alteration in composition of the polypeptide encoded by a protein kinase, or for the presence of a particular variant encoded by a protein kinase. An alteration in expression of a polypeptide encoded by a protein kinase can be, for example, an alteration in the quantitative polypeptide expression (*i.e.*, the amount of polypeptide produced); an alteration in the composition of a polypeptide encoded by a protein kinase is an alteration in the qualitative polypeptide expression (*e.g.*, expression of a mutant protein kinase polypeptide or of a different splicing variant). In a preferred embodiment, diagnosis of susceptibility to a disease or condition associated with a protein kinase is made by detecting a particular splicing variant encoded by that protein kinase, or a particular pattern of splicing variants.

Both such alterations (quantitative and qualitative) can also be present. An “alteration” in the polypeptide expression or composition, as used herein, refers to an alteration in expression or composition in a test sample, as compared with the expression or composition of polypeptide by a protein kinase in a control sample. A control sample is a sample that corresponds to the test sample (*e.g.*, is from the same type of cells), and is from an individual who is not affected by a susceptibility to a disease or condition associated with a protein kinase. An alteration in the expression or composition of the polypeptide in the test sample, as compared with the control sample, is indicative of a susceptibility to a disease or condition associated with a protein kinase. Similarly, the presence of one or more different splicing variants in the test sample, or the presence of significantly different amounts of different splicing variants in the test sample, as compared with the control sample, is indicative of a susceptibility to a disease or condition associated with a protein kinase. Various means of examining expression or composition of the polypeptide encoded by a protein kinase can be used, including spectroscopy, colorimetry, electrophoresis, isoelectric focusing, and immunoassays (*e.g.*, David *et al.*, U.S. Pat. No. 4,376,110) such as immunoblotting (see also *Current Protocols in Molecular Biology*, particularly Chapter 10). For example, in one embodiment, an antibody capable of binding to the polypeptide (*e.g.*, as described above), preferably an antibody with a detectable label, can be used. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The term “labeled”, with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

Western blotting analysis, using an antibody as described above that specifically binds to a polypeptide encoded by a mutant protein kinase, or an antibody that specifically binds to a polypeptide encoded by a non-mutant gene, or an antibody that specifically binds to a particular splicing variant encoded by a protein kinase, can be used to identify the presence in a test sample of a particular splicing variant or of a polypeptide encoded by a polymorphic or mutant protein kinase, or the absence in a test sample of a particular splicing variant or of a

polypeptide encoded by a non-polymorphic or non-mutant gene. The presence of a polypeptide encoded by a polymorphic or mutant gene, or the absence of a polypeptide encoded by a non-polymorphic or non-mutant gene, is diagnostic for a susceptibility to a disease or condition associated with a protein kinase, as is the presence (or absence) of particular splicing variants encoded by the protein kinase gene.

In one embodiment of this method, the level or amount of polypeptide encoded by a protein kinase in a test sample is compared with the level or amount of the polypeptide encoded by the protein kinase in a control sample. A level or amount of the polypeptide in the test sample that is higher or lower than the level or amount of the polypeptide in the control sample, such that the difference is statistically significant, is indicative of an alteration in the expression of the polypeptide encoded by the protein kinase, and is diagnostic for a susceptibility to a disease or condition associated with that protein kinase.

Alternatively, the composition of the polypeptide encoded by a protein kinase in a test sample is compared with the composition of the polypeptide encoded by the protein kinase in a control sample (*e.g.*, the presence of different splicing variants). A difference in the composition of the polypeptide in the test sample, as compared with the composition of the polypeptide in the control sample, is diagnostic for a susceptibility to a disease or condition associated with that protein kinase. In another embodiment, both the level or amount and the composition of the polypeptide can be assessed in the test sample and in the control sample. A difference in the amount or level of the polypeptide in the test sample, compared to the control sample; a difference in composition in the test sample, compared to the control sample; or both a difference in the amount or level, and a difference in the composition, is indicative of a susceptibility to a disease or condition associated with that protein kinase.

Kits (*e.g.*, reagent kits) useful in the methods of diagnosis comprise components useful in any of the methods described herein, including for example, hybridization probes or primers as described herein (*e.g.*, labeled probes or primers), reagents for detection of labeled molecules, restriction enzymes (*e.g.*, for RFLP analysis), allele-specific oligonucleotides, antibodies which bind to mutant or to non-mutant (native) protein kinase polypeptide, means for amplification of nucleic acids comprising a protein kinase, or means for analyzing the nucleic acid sequence of a protein kinase or for analyzing the amino acid sequence of a protein kinase polypeptide, etc.

SCREENING ASSAYS AND AGENTS IDENTIFIED THEREBY

The invention provides methods (also referred to herein as “screening assays”) for identifying the presence of a nucleotide that hybridizes to a nucleic acid of the invention, as well as for identifying the presence of a polypeptide encoded by a nucleic acid of the invention. In one embodiment, the presence (or absence) of a nucleic acid molecule of interest (*e.g.*, a nucleic acid that has significant homology with a nucleic acid of the invention) in a sample can be assessed by contacting the sample with a nucleic acid comprising a nucleic acid of the invention (*e.g.*, a nucleic acid having the sequence of one of SEQ ID NOs: 1-80 (odd numbers), or the complement thereof, or a nucleic acid encoding an amino acid having the sequence of one of SEQ ID NOs: 1-80 (odd numbers), or a fragment or variant of such nucleic acids), under stringent conditions as described above, and then assessing the sample for the presence (or absence) of hybridization. In a preferred embodiment, high stringency conditions are conditions appropriate for selective hybridization. In another embodiment, a sample containing the nucleic acid molecule of interest is contacted with a nucleic acid containing a contiguous nucleotide sequence (*e.g.*, a primer or a probe as described above) that is at least partially complementary to a part of the nucleic acid molecule of interest (*e.g.*, a protein kinase nucleic acid), and the contacted sample is assessed for the presence or absence of hybridization. In a preferred embodiment, the nucleic acid containing a contiguous nucleotide sequence is completely complementary to a part of the nucleic acid molecule of interest.

In any of these embodiments, all or a portion of the nucleic acid of interest can be subjected to amplification prior to performing the hybridization.

In another embodiment, the presence (or absence) of a polypeptide of interest, such as a polypeptide of the invention or a fragment or variant thereof, in a sample can be assessed by contacting the sample with an antibody that specifically hybridizes to the polypeptide of interest (*e.g.*, an antibody such as those described above), and then assessing the sample for the presence (or absence) of binding of the antibody to the polypeptide of interest.

In another embodiment, the invention provides methods for identifying agents (*e.g.*, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes which alter (*e.g.*, increase or decrease) the activity of the polypeptides described herein, or which otherwise interact with the polypeptides herein. For example, such agents can be agents which bind to polypeptides described herein (*e.g.*, protein kinase binding

agents); which have a stimulatory or inhibitory effect on, for example, activity of polypeptides of the invention; or which change (*e.g.*, enhance or inhibit) the ability of the polypeptides of the invention to interact with protein kinase binding agents (*e.g.*, receptors or other binding agents); or which alter posttranslational processing of the protein kinase polypeptide (*e.g.*, agents that alter proteolytic processing to direct the polypeptide from where it is normally synthesized to another location in the cell, such as the cell surface; agents that alter proteolytic processing such that more polypeptide is released from the cell, etc.

In one embodiment, the invention provides assays for screening candidate or test agents that bind to or modulate the activity of polypeptides described herein (or biologically active portion(s) thereof), as well as agents identifiable by the assays. Test agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S., *Anticancer Drug Des.* 12:145 (1997)).

In one embodiment, to identify agents which alter the activity of a protein kinase polypeptide, a cell, cell lysate, or solution containing or expressing a protein kinase polypeptide (*e.g.*, one of SEQ ID NOs: 1-80 (odd numbers), or another splicing variant encoded by a protein kinase), or a fragment or derivative thereof (as described above), can be contacted with an agent to be tested; alternatively, the polypeptide can be contacted directly with the agent to be tested. The level (amount) of protein kinase activity is assessed (*e.g.*, the level (amount) of protein kinase activity is measured, either directly or indirectly), and is compared with the level of activity in a control (*i.e.*, the level of activity of the protein kinase polypeptide or active fragment or derivative thereof in the absence of the agent to be tested). If the level of the activity in the presence of the agent differs, by an amount that is statistically significant, from the level of the activity in the absence of the agent, then the agent is an agent that alters the activity of a protein kinase polypeptide. An increase in the level of protein kinase activity relative to a control, indicates that the agent is an agent that enhances (is an agonist of) protein kinase activity. Similarly, a decrease in the level of protein kinase activity relative to a control, indicates that the agent is an agent that inhibits (is an antagonist of) protein

kinase activity. In another embodiment, the level of activity of a protein kinase polypeptide or derivative or fragment thereof in the presence of the agent to be tested, is compared with a control level that has previously been established. A level of the activity in the presence of the agent that differs from the control level by an amount that is statistically significant indicates that the agent alters protein kinase activity.

The present invention also relates to an assay for identifying agents which alter the expression of a protein kinase gene (*e.g.*, antisense nucleic acids, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes) which alter (*e.g.*, increase or decrease) expression (*e.g.*, transcription or translation) of the gene or which otherwise interact with the nucleic acids described herein, as well as agents identifiable by the assays. For example, a solution containing a nucleic acid encoding a protein kinase polypeptide (*e.g.*, a protein kinase gene) can be contacted with an agent to be tested. The solution can comprise, for example, cells containing the nucleic acid or cell lysate containing the nucleic acid; alternatively, the solution can be another solution that comprises elements necessary for transcription/translation of the nucleic acid. Cells not suspended in solution can also be employed, if desired. The level and/or pattern of protein kinase expression (*e.g.*, the level and/or pattern of mRNA or of protein expressed, such as the level and/or pattern of different splicing variants) is assessed, and is compared with the level and/or pattern of expression in a control (*i.e.*, the level and/or pattern of the protein kinase expression in the absence of the agent to be tested). If the level and/or pattern in the presence of the agent differ, by an amount or in a manner that is statistically significant, from the level and/or pattern in the absence of the agent, then the agent is an agent that alters the expression of a protein kinase. Enhancement of protein kinase expression indicates that the agent is an agonist of protein kinase activity. Similarly, inhibition of protein kinase expression indicates that the agent is an antagonist of protein kinase activity. In another embodiment, the level and/or pattern of protein kinase polypeptide(s) (*e.g.*, different splicing variants) in the presence of the agent to be tested, is compared with a control level and/or pattern that have previously been established. A level and/or pattern in the presence of the agent that differs from the control level and/or pattern by an amount or in a manner that is statistically significant indicates that the agent alters protein kinase expression.

In another embodiment of the invention, agents which alter the expression of a protein kinase gene or which otherwise interact with the nucleic acids described herein, can be identified using a cell, cell lysate, or solution containing a nucleic acid encoding the promoter region of the protein kinase gene operably linked to a reporter gene. After contact with an agent to be tested, the level of expression of the reporter gene (*e.g.*, the level of mRNA or of protein expressed) is assessed, and is compared with the level of expression in a control (*i.e.*, the level of the expression of the reporter gene in the absence of the agent to be tested). If the level in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters the expression of the protein kinase, as indicated by its ability to alter expression of a gene that is operably linked to the protein kinase gene promoter. Enhancement of the expression of the reporter indicates that the agent is an agonist of protein kinase activity. Similarly, inhibition of the expression of the reporter indicates that the agent is an antagonist of protein kinase activity. In another embodiment, the level of expression of the reporter in the presence of the agent to be tested, is compared with a control level that has previously been established. A level in the presence of the agent that differs from the control level by an amount or in a manner that is statistically significant indicates that the agent alters f expression.

Agents which alter the amounts of different splicing variants encoded by a protein kinase (*e.g.*, an agent which enhances activity of a first splicing variant, and which inhibits activity of a second splicing variant), as well as agents which are agonists of activity of a first splicing variant and antagonists of activity of a second splicing variant, can easily be identified using these methods described above.

In other embodiments of the invention, assays can be used to assess the impact of a test agent on the activity of a polypeptide in relation to a protein kinase binding agent. For example, a cell that expresses a compound that interacts with a protein kinase (herein referred to as a "protein kinase binding agent", which can be a polypeptide or other molecule that interacts with a protein kinase, such as a receptor) is contacted with a protein kinase in the presence of a test agent, and the ability of the test agent to alter the interaction between the protein kinase and the protein kinase binding agent is determined. Alternatively, a cell lysate or a solution containing the protein kinase binding agent, can be used. An agent which binds to the protein kinase or the protein kinase binding agent can alter the interaction by interfering with, or enhancing the ability of the protein kinase to bind to, associate with, or otherwise interact with the protein kinase binding agent. Determining the

ability of the test agent to bind to a protein kinase or a protein kinase binding agent can be accomplished, for example, by coupling the test agent with a radioisotope or enzymatic label such that binding of the test agent to the polypeptide can be determined by detecting the labeled with ^{125}I , ^{35}S , ^{14}C or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemmission or by scintillation counting. Alternatively, test agents can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. It is also within the scope of this invention to determine the ability of a test agent to interact with the polypeptide without the labeling of any of the interactants. For example, a microphysiometer can be used to detect the interaction of a test agent with a protein kinase or a protein kinase binding agent without the labeling of either the test agent, protein kinase, or the protein kinase binding agent. McConnell, H.M. *et al.*, *Science* 257:1906-1912 (1992). As used herein, a “microphysiometer” (*e.g.*, Cytosensor™) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between ligand and polypeptide. Thus, these receptors can be used to screen for compounds that are agonists for use in treating a susceptibility to a disease or condition associated with a protein kinase or antagonists for studying a susceptibility to a disease or condition associated with a protein kinase. Drugs could be designed to regulate protein kinase activation that in turn can be used to regulate signaling pathways and transcription events of genes downstream.

In another embodiment of the invention, assays can be used to identify polypeptides that interact with one or more protein kinase polypeptides, as described herein. For example, a yeast two-hybrid system such as that described by Fields and Song (Fields, S. and Song, O., *Nature* 340:245-246 (1989)) can be used to identify polypeptides that interact with one or more protein kinase polypeptides. In such a yeast two-hybrid system, vectors are constructed based on the flexibility of a transcription factor that has two functional domains (a DNA binding domain and a transcription activation domain). If the two domains are separated but fused to two different proteins that interact with one another, transcriptional activation can be achieved, and transcription of specific markers (*e.g.*, nutritional markers such as His and Ade, or color markers such as lacZ) can be used to identify the presence of interaction and transcriptional activation. For example, in the methods of the

invention, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also a protein kinase polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the protein kinase polypeptide, splicing variant, or fragment or derivative thereof (*e.g.*, a protein kinase polypeptide binding agent or receptor). Incubation of yeast containing the first vector and the second vector under appropriate conditions (*e.g.*, mating conditions such as used in the Matchmaker™ system from Clontech (Palo Alto, California, USA)) allows identification of colonies that express the markers of interest. These colonies can be examined to identify the polypeptide(s) that interact with the protein kinase polypeptide or fragment or derivative thereof. Such polypeptides may be useful as agents that alter the activity of expression of a protein kinase polypeptide, as described above.

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either the protein kinase, the protein kinase binding agent, or other components of the assay on a solid support, in order to facilitate separation of complexed from uncomplexed forms of one or both of the polypeptides, as well as to accommodate automation of the assay. Binding of a test agent to the polypeptide, or interaction of the polypeptide with a binding agent in the presence and absence of a test agent, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein (*e.g.*, a glutathione-S-transferase fusion protein) can be provided which adds a domain that allows a protein kinase or a protein kinase binding agent to be bound to a matrix or other solid support.

In another embodiment, modulators of expression of nucleic acid molecules of the invention are identified in a method wherein a cell, cell lysate, or solution containing a nucleic acid encoding a protein kinase is contacted with a test agent and the expression of appropriate mRNA or polypeptide (*e.g.*, splicing variant(s)) in the cell, cell lysate, or solution, is determined. The level of expression of appropriate mRNA or polypeptide(s) in the presence of the test agent is compared to the level of expression of mRNA or polypeptide(s) in the absence of the test agent. The test agent can then be identified as a modulator of expression based on this comparison. For example, when expression of mRNA or polypeptide is greater (statistically significantly greater) in the presence of the test agent than in its absence, the test

agent is identified as a stimulator or enhancer of the mRNA or polypeptide expression. Alternatively, when expression of the mRNA or polypeptide is less (statistically significantly less) in the presence of the test agent than in its absence, the test agent is identified as an inhibitor of the mRNA or polypeptide expression. The level of mRNA or polypeptide expression in the cells can be determined by methods described herein for detecting mRNA or polypeptide.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a test agent that is a modulating agent, an antisense nucleic acid molecule, a specific antibody, or a polypeptide-binding agent) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein. In addition, an agent identified as described herein can be used to alter activity of a polypeptide encoded by a protein kinase, or to alter expression of a protein kinase, by contacting the polypeptide or the gene (or contacting a cell comprising the polypeptide or the gene) with the agent identified as described herein.

PHARMACEUTICAL COMPOSITIONS

The present invention also pertains to pharmaceutical compositions comprising nucleic acids described herein, particularly nucleotides encoding the polypeptides described herein; comprising polypeptides described herein (*e.g.*, one or more of SEQ ID NOs: 1-80 (even numbers)); and/or comprising other splicing variants encoded by a protein kinase; and/or an agent that alters (*e.g.*, enhances or inhibits) protein kinase gene expression or protein kinase polypeptide activity as described herein. For instance, a polypeptide, protein (*e.g.*, a protein kinase receptor), an agent that alters protein kinase gene expression, or a protein kinase binding agent or binding partner, fragment, fusion protein or prodrug thereof, or a nucleotide or nucleic acid construct (vector) comprising a nucleotide of the present invention, or an agent that alters protein kinase polypeptide activity, can be formulated with a physiologically acceptable carrier or excipient to prepare a

pharmaceutical composition. The carrier and composition can be sterile. The formulation should suit the mode of administration.

Suitable pharmaceutically acceptable carriers include but are not limited to water, salt solutions (*e.g.*, NaCl), saline, buffered saline, alcohols, glycerol, ethanol, gum arabic, vegetable oils, benzyl alcohols, polyethylene glycols, gelatin, carbohydrates such as lactose, amylose or starch, dextrose, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid esters, hydroxymethylcellulose, polyvinyl pyrrolidone, etc., as well as combinations thereof. The pharmaceutical preparations can, if desired, be mixed with auxiliary agents, *e.g.*, lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, flavoring and/or aromatic substances and the like which do not deleteriously react with the active agents.

The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, polyvinyl pyrrolidone, sodium saccharine, cellulose, magnesium carbonate, etc.

Methods of introduction of these compositions include, but are not limited to, intradermal, intramuscular, intraperitoneal, intraocular, intravenous, subcutaneous, topical, oral and intranasal. Other suitable methods of introduction can also include gene therapy (as described below), rechargeable or biodegradable devices, particle acceleration devices ("gene guns") and slow release polymeric devices. The pharmaceutical compositions of this invention can also be administered as part of a combinatorial therapy with other agents.

The composition can be formulated in accordance with the routine procedures as a pharmaceutical composition adapted for administration to human beings. For example, compositions for intravenous administration typically are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be

dispensed with an infusion bottle containing sterile pharmaceutical grade water, saline or dextrose/water. Where the composition is administered by injection, an ampule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

5 For topical application, nonsprayable forms, viscous to semi-solid or solid forms comprising a carrier compatible with topical application and having a dynamic viscosity preferably greater than water, can be employed. Suitable formulations include but are not limited to solutions, suspensions, emulsions, creams, ointments, powders, enemas, lotions, sols, liniments, salves, aerosols, etc.,
10 which are, if desired, sterilized or mixed with auxiliary agents, *e.g.*, preservatives, stabilizers, wetting agents, buffers or salts for influencing osmotic pressure, etc. The agent may be incorporated into a cosmetic formulation. For topical application, also suitable are sprayable aerosol preparations wherein the active ingredient, preferably in combination with a solid or liquid inert carrier material, is packaged in a squeeze
15 bottle or in admixture with a pressurized volatile, normally gaseous propellant, *e.g.*, pressurized air.

Agents described herein can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc.,
20 and those formed with free carboxyl groups such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The agents are administered in a therapeutically effective amount. The amount of agents which will be therapeutically effective in the treatment of a
25 particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the symptoms of a susceptibility to a
30 disease or condition associated with a protein kinase, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

35 The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a

notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use of sale for human administration. The pack or kit can be labeled with information regarding mode of administration, sequence of drug administration (*e.g.*, separately, sequentially or concurrently), or the like. The pack or kit may also include means for reminding the patient to take the therapy. The pack or kit can be a single unit dosage of the combination therapy or it can be a plurality of unit dosages. In particular, the agents can be separated, mixed together in any combination, present in a single vial or tablet. Agents assembled in a blister pack or other dispensing means is preferred. For the purpose of this invention, unit dosage is intended to mean a dosage that is dependent on the individual pharmacodynamics of each agent and administered in FDA approved dosages in standard time courses.

METHODS OF THERAPY

The present invention also pertains to methods of treatment (prophylactic and/or therapeutic) for a susceptibility to a disease or condition associated with a protein kinase, using a protein kinase therapeutic agent. A “protein kinase therapeutic agent” is an agent that alters (*e.g.*, enhances or inhibits) protein kinase polypeptide activity and/or protein kinase gene expression, as described herein (*e.g.*, a protein kinase agonist or antagonist). Protein kinase therapeutic agents can alter protein kinase polypeptide activity or gene expression by a variety of means, such as, for example, by providing additional protein kinase polypeptide or by upregulating the transcription or translation of the protein kinase gene; by altering posttranslational processing of the protein kinase polypeptide; by altering transcription of protein kinase splicing variants; or by interfering with protein kinase polypeptide activity (*e.g.*, by binding to a protein kinase polypeptide), or by downregulating the transcription or translation of a protein kinase gene. Representative protein kinase therapeutic agents include the following:

nucleic acids or fragments or derivatives thereof described herein, particularly nucleotides encoding the polypeptides described herein and vectors comprising such nucleic acids (*e.g.*, a gene, cDNA, and/or mRNA, such as a nucleic acid encoding a protein kinase polypeptide or active fragment or derivative thereof, or an oligonucleotide; for example, one of SEQ ID NOs: 1-80 (odd numbers), or a complement thereof, or a nucleic acid encoding one of SEQ ID NOs: 1-80 (odd numbers), or fragments or derivatives thereof);

polypeptides described herein (*e.g.*, one or more of SEQ ID NOs: 1-80 (even numbers), and/or other splicing variants encoded by a protein kinase, or fragments or derivatives thereof);

5 other polypeptides (*e.g.*, protein kinase receptors); protein kinase binding agents; peptidomimetics; fusion proteins or prodrugs thereof; antibodies (*e.g.*, an antibody to a mutant protein kinase polypeptide, or an antibody to a non-mutant protein kinase polypeptide, or an antibody to a particular splicing variant encoded by a protein kinase, as described above); ribozymes; other small molecules; and

10 other agents that alter (*e.g.*, enhance or inhibit) protein kinase gene expression or polypeptide activity, or that regulate transcription of protein kinase splicing variants (*e.g.*, agents that affect which splicing variants are expressed, or that affect the amount of each splicing variant that is expressed.

More than one protein kinase therapeutic agent can be used concurrently, if desired.

15 A protein kinase therapeutic agent that is a nucleic acid is used in the treatment of a susceptibility to a disease or condition associated with a protein kinase. The term, "treatment" as used herein, refers not only to ameliorating symptoms associated with the disease, but also preventing or delaying the onset of the disease, and also lessening the severity or frequency of symptoms of the disease.
20 The therapy is designed to alter (*e.g.*, inhibit or enhance), replace or supplement activity of a protein kinase polypeptide in an individual. For example, a protein kinase therapeutic agent can be administered in order to upregulate or increase the expression or availability of the protein kinase gene or of specific splicing variants of protein kinase, or, conversely, to downregulate or decrease the expression or
25 availability of the protein kinase gene or specific splicing variants of the protein kinase. Upregulation or increasing expression or availability of a native protein kinase gene or of a particular splicing variant could interfere with or compensate for the expression or activity of a defective gene or another splicing variant; downregulation or decreasing expression or availability of a native protein kinase
30 gene or of a particular splicing variant could minimize the expression or activity of a defective gene or the particular splicing variant and thereby minimize the impact of the defective gene or the particular splicing variant.

35 The protein kinase therapeutic agent(s) are administered in a therapeutically effective amount (*i.e.*, an amount that is sufficient to treat the disease, such as by ameliorating symptoms associated with the disease, preventing or delaying the onset of the disease, and/or also lessening the severity or frequency of symptoms of the

disease). The amount which will be therapeutically effective in the treatment of a particular individual's disorder or condition will depend on the symptoms and severity of the disease, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

In one embodiment, a nucleic acid of the invention (*e.g.*, a nucleic acid encoding a protein kinase polypeptide, such as one of SEQ ID NOs: 1-80 (even numbers), or a complement thereof; or another nucleic acid that encodes a protein kinase polypeptide or a splicing variant, derivative or fragment thereof, such as a nucleic acid encoding one of SEQ ID NOs: 1-80 (odd numbers)) can be used, either alone or in a pharmaceutical composition as described above. For example, a protein kinase or a cDNA encoding a protein kinase polypeptide, either by itself or included within a vector, can be introduced into cells (either *in vitro* or *in vivo*) such that the cells produce native protein kinase polypeptide. If necessary, cells that have been transformed with the gene or cDNA or a vector comprising the gene or cDNA can be introduced (or re-introduced) into an individual affected with the disease. Thus, cells which, in nature, lack native protein kinase expression and activity, or have mutant protein kinase expression and activity, or have expression of a disease-associated protein kinase splicing variant, can be engineered to express the protein kinase polypeptide or an active fragment of the protein kinase polypeptide (or a different variant of the protein kinase polypeptide). In a preferred embodiment, nucleic acid encoding a protein kinase polypeptide, or an active fragment or derivative thereof, can be introduced into an expression vector, such as a viral vector, and the vector can be introduced into appropriate cells in an animal. Other gene transfer systems, including viral and nonviral transfer systems, can be used. Alternatively, nonviral gene transfer methods, such as calcium phosphate coprecipitation, mechanical techniques (*e.g.*, microinjection); membrane fusion-mediated transfer via liposomes; or direct DNA uptake, can also be used.

Alternatively, in another embodiment of the invention, a nucleic acid of the invention; a nucleic acid complementary to a nucleic acid of the invention; or a portion of such a nucleic acid (*e.g.*, an oligonucleotide as described below), can be used in "antisense" therapy, in which a nucleic acid (*e.g.*, an oligonucleotide) which

specifically hybridizes to the mRNA and/or genomic DNA of a protein kinase is administered or generated *in situ*. The antisense nucleic acid that specifically hybridizes to the mRNA and/or DNA inhibits expression of the protein kinase polypeptide, *e.g.*, by inhibiting translation and/or transcription. Binding of the antisense nucleic acid can be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interaction in the major groove of the double helix.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid as described above. When the plasmid is transcribed in the cell, it produces RNA that is complementary to a portion of the mRNA and/or DNA which encodes the protein kinase polypeptide. Alternatively, the antisense construct can be an oligonucleotide probe that is generated *ex vivo* and introduced into cells; it then inhibits expression by hybridizing with the mRNA and/or genomic DNA of the protein kinase. In one embodiment, the oligonucleotide probes are modified oligonucleotides which are resistant to endogenous nucleases, *e.g.*, exonucleases and/or endonucleases, thereby rendering them stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Pat. Nos. 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy are also described, for example, by Van der Krol *et al.* (*Biotechniques* 6:958-976 (1988)); and Stein *et al.* (*Cancer Res.* 48:2659-2668 (1988)). With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site are preferred.

To perform antisense therapy, oligonucleotides (mRNA, cDNA or DNA) are designed that are complementary to mRNA encoding the protein kinase. The antisense oligonucleotides bind to protein kinase mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, indicates that a sequence has sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid, as described in detail above. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as

the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures.

The oligonucleotides used in antisense therapy can be DNA, RNA, or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotides can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotides can include other appended groups such as peptides (*e.g.* for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA* 86:6553-6556 (1989); Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 84:648-652 (1987); PCT International Publication No. WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT International Publication No. WO 89/10134), or hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, *BioTechniques* 6:958-976 (1988)) or intercalating agents. (See, *e.g.*, Zon, *Pharm. Res.* 5:539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule (*e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent).

The antisense molecules are delivered to cells which express protein kinase *in vivo*. A number of methods can be used for delivering antisense DNA or RNA to cells; *e.g.*, antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systemically. Alternatively, in a preferred embodiment, a recombinant DNA construct is utilized in which the antisense oligonucleotide is placed under the control of a strong promoter (*e.g.*, pol III or pol II). The use of such a construct to transfect target cells in the patient results in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous protein kinase transcripts and thereby prevent translation of the protein kinase mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art and described above. For example, a plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct that can be introduced directly into the tissue site. Alternatively, viral vectors can be used which selectively

infect the desired tissue, in which case administration may be accomplished by another route (*e.g.*, systemically).

Endogenous protein kinase expression can also be reduced by inactivating or “knocking out” protein kinase or its promoter using targeted homologous recombination (*e.g.*, see Smithies *et al.*, *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson *et al.*, *Cell* 5:313-321 (1989)). For example, a mutant, non-functional protein kinase (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous protein kinase (either the coding regions or regulatory regions of protein kinase) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the protein kinase *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the protein kinase. The recombinant DNA constructs can be directly administered or targeted to the required site *in vivo* using appropriate vectors, as described above. Alternatively, expression of non-mutant protein kinases can be increased using a similar method: targeted homologous recombination can be used to insert a DNA construct comprising a non-mutant, functional protein kinase, *e.g.*, a gene having one of SEQ ID NOs: 1-80 (odd numbers), or the complement thereof, or a portion thereof, in place of a mutant protein kinase in the cell, as described above. In another embodiment, targeted homologous recombination can be used to insert a DNA construct comprising a nucleic acid that encodes a protein kinase polypeptide variant that differs from that present in the cell.

Alternatively, endogenous protein kinase expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of a protein kinase (*i.e.*, the protein kinase promoter and/or enhancers) to form triple helical structures that prevent transcription of the protein kinase in target cells in the body. (See generally, Helene, C., *Anticancer Drug Des.*, 6(6):569-84 (1991); Helene, C. *et al.*, *Ann. N.Y. Acad. Sci.* 660:27-36 (1992); and Maher, L. J., *Bioassays* 14(12):807-15 (1992)). Likewise, the antisense constructs described herein, by antagonizing the normal biological activity of one of the protein kinase proteins, can be used in the manipulation of tissue, *e.g.*, tissue differentiation, both *in vivo* and *for ex vivo* tissue cultures. Furthermore, the anti-sense techniques (*e.g.*, microinjection of antisense molecules, or transfection with plasmids whose transcripts are anti-sense with regard to a protein kinase mRNA or gene sequence) can be used to investigate the role of one or protein kinase in developmental events, as well as the

normal cellular function of the protein kinases in adult tissue. Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals.

In yet another embodiment of the invention, other protein kinase therapeutic agents as described herein can also be used in the treatment or prevention of a susceptibility to a disease or condition associated with a protein kinase. The therapeutic agents can be delivered in a composition, as described above, or by themselves. They can be administered systemically, or can be targeted to a particular tissue. The therapeutic agents can be produced by a variety of means, including chemical synthesis; recombinant production; *in vivo* production (*e.g.*, a transgenic animal, such as U.S. Pat. No. 4,873,316 to Meade *et al.*), for example, and can be isolated using standard means such as those described herein.

A combination of any of the above methods of treatment (*e.g.*, administration of non-mutant protein kinase polypeptide in conjunction with antisense therapy targeting mutant protein kinase mRNA; administration of a first splicing variant encoded by a protein kinase in conjunction with antisense therapy targeting a second splicing encoded by a protein kinase) can also be used.

The teachings of all publications cited herein are incorporated herein by reference in their entirety.

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the scope of the invention encompassed by the appended claims.

Table I

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MOOSE03177 ctg16439 524311..524473, 539059..539119, 569811..569849,
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 20 AKSVPTKTYSNVTLWYRPPDVLLGSTYEYSTPIDMWSCGCIRCCMFEEELK
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MOOSE03219 ctg17937 2644450..2644580, 2645668..2645883,
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MOOSE03288 ctg17685 34737..34809, 70525..70657, 76156..76460,
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MOOSE03296 ctg15131 27531456..27531520, 27535488..27535536,
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 NO: 16)

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MOOSE03304 ctg16704 2286265..2286402, 2292680..2292937,
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 19)

MOOSE03306 ctg19011 264101..264248, 274458..274708,
 289937..290629

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 15 gcagtgccatggtgtacaacttagccaatgccctcaggtatctccatggcctcagcatcgtgcacagagacatcaaacca
 gagaatctcttggtgtgaatatcctgatggaaccaagctcttgaaactgggagactttgggcttgactgtggtagaag
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 20 aatcagtcaaagtcttcaggtaaatgttgaaagctcgggtgaccgcgggacaaatcctgagtcaccctgggtgtaccaat
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 aatcagacctgccaaggtgatgggcgtctgagttcacatctggccccccaccctgtctctacagaaaaaaaaatTTTT
 25 tttcaaaattcatggcagccactaaccacgtggctgttaacactggaaatgtccctgtccaaactgagacatgctataaa
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MOOSE03313 ctg595 6983799..6984235, 7002305..7003166

DAAVLKRRGYLLGINLGEFSYAKVKSAYSERLKFNVAIKIIDRKKAPA
 30 DFLEKFLPREIEILAMLNHCSIKTIEIFETSHGKVYIVMELAVQGDILLELIKT
 RGALHEDEARKKFHQLSLAIKYCHDLDVVHRDLKCDNLLDKDFNIKLSDF
 SFSKRCLRDDSGRMALSKTFCGSPAYAAPEVLQGIPYQPKVYDIWSLGVILY
 IMVCGSMPYDDSDNIKKMLRIQKEHRVNFPRSKHLTGECKDLIYHMLQPDVN
 35 RRLHIDEILSHCWMQPKARGSPSVAINKEGENKTTKMGRNQSRKAENSKNQ
 SAFSPPKDHSSSPAMEQSWTENDFDKLTEVGFRRSVITNFSKLKEDVRTHHK
 EAKSLEKRLDQWLNRRINSVEETLNDLMELKTMARELRDACTRFNSQFDQVE
 ERVSVIEDQINEIKQEEKVREKS (SEQ ID NO: 28)

gacgctgctgtcctcaagcgacgagggtacctcctggggataaatttaggagaggggtcctatgcaaaagtaaa
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 40 agaaattccttccccgggaaattgagattctggccatgttaaaccactgctccatcataagacctacgagatctttgagac
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 45 cctgcgggatgacagtggctgaatggccttaagcaagaccttctgtgggtcaccagcgtatcgggccccagaggtgctg
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 accaatggctaaatagaataaacagtgtagaggagaccttaaatgacctgatggagctgaaaacctggcagcagaact
 5 acgtgacgcatgcacaagatttaataagccaattcgatcaagtggagaagggtatcagtgattgaagatcaaattaatga
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MOOSE03314 ctg595 6468110..6468440, 6516667..6517550
 DAAVLKRRGYLLGINLGESYAKVKSAYSERLKFNVAIKIIDRKKAPA
 10 DFLEKFLPREIEILAMLNHCSIKTIEIFETSHGKVYIVMELAVQGDILLELIK
 RGALHEDEARKKFHQLSLAIKYCHDLDVHRDLKCDNLLLDKDFNIKLSDF
 SFSKRCLRDDSGRMALSKTFCGSPAYAAPEVLQIPYQPKVYDIWSLGVILY
 IMVCGSMPYDDSDNIKKMLRIQKEHRVNFPRSKHLTGECKDLIYHMLQPDVN
 RRLHIDEILSHCWMQPKARGSPSVAINKEGESSRGTEPLTEVITNSLSDHSGI
 15 KLKLTIKLKTQNCTTSWNLNNNVLLNDYWVNNEIKAEIKFFETNENKDTSY
 QNLWTLAKAVFRGKFIELNAHKRKQERSKIDTLTSQLKELESRA (SEQ ID
 NO: 30)

gacgctgctgtcctcaagcgacgaggctacctcctggggataaatttaggagagggctcctatgcaaaagtaaa
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 20 agaaattccttccccgggaaattgagattctggccatgttaaaccactgctccatcataagacctacgagatctttgagac
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 25 cagggcattcctaccagcccaaggtgtacgacatctggagcctaggcgtgatcctctacatcatggctgtcggtccat
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 30 aaactcactcaaaactgcacaacctcatggaacctgaacaacaacgtgctcctgaatgactactgggtaataaacgaaatt
 aaggcagaaataattaagttctttgaaaccaatgagaacaaagacacatcataccagaatctctggacactagctaaagc
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 aattaaaggaactagaaagcagagca (SEQ ID NO: 29)

MOOSE03316 ctg22fin3 2266883..2267851, 2269136..2269261
 DATVLRKKGYIVGINLGKGSYAKVKSAYSERLKFNVAVKIIDRKKTPT
 35 DFVERFLPREMDILATVNHGSIKTIEIFETSDGRIYIIMELGVQGDILLEFIKQ
 GALHEDVARKMFRQLSSAVKYCHDLDIVHRDLKCENLLLDKDFNIKLSDFG
 FSKRCLRDSNGRIILSKTFCGSAAYAAPEVLQSIPYQPKVYDIWSLGVILYIM
 40 VCGSMPYDDSDIRKMLRIQKEHRVDFPRSKNLTCECKDLIYRMLQPDVSQR
 LHIDEILSHSWLQPPKPKATSSASFKREGEGKYRAECKLDTKTGLRPDHRPD
 HKLGAKTQHRLLVGNLRVQLPRAPFLHIPPEKQKALQDVSSTQNTGSECR
 RKQR (SEQ ID NO: 32)

gatgccacagtcctaaggaagaagggttacatcgtaggcatcaatcttggaagggttctacgcaaaagtcaa
 45 atctgcctactctgagcgctcaagtcaatgtggctgtcaagatcatcgaccgcaagaaaacacctactgacttttgga
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10 (SEQ ID NO: 31)

MOOSE03330 ctg14489 3270126..3270273, 3271022..3271654,
3272933..3272941, 3276338..3276388, 3288738..3288805, 3332756..3332897,
3349729..3349937

15 SMEDFLLSNGYQLGKTIGEGTYSKVKEAFSKKHQRKVAIKVIDKMGG
PEEFIQRFLPRELQIVRTL D HKNIIQVYEMLESADGKICLVMELAEAGGDV FDC
VLNGGPLPESRAKALFRQMVEAIRYCHGCGVAHRDLKCENALLQGFNLKL
TDFGFAKVLPKSHRELSQTF CGSTAYAAPEVLQIPHDSKKGDVWSMGVVL
YVMLCASLPFDDTDIPKMLWQQQKGVSFPT HLSISADCQDLLKRLLPE DMIL
20 RPSIEEVKQHRWFQTPDLNDLATSASQDTGHRKHPFSARILSQPQSSFSLEIQ
NAELASPAHWGKVQPPQEDLEAQLGSLGGLQKVSSPQGALVSELAMEMQS
YYAKLLGELNEQRKRDFFCDCSIIIVEGRIFKAHRNILFANSGYFRALLIHYIQ
DSGRHSTASLD (SEQ ID NO: 34)

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25 caaagaagcattttcaaaaaacaccaaaagaaagtggcaattaaagttatagacaagatgggagggccagaagagttt
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40 33)

MOOSE03332 ctg15907 2781758..2781942, 2783326..2783392,
2824027..2824141, 2827236..2827388, 2828296..2828408, 2829233..2829307,
2832037..2832178, 2834312..2834421, 2834490..2834592, 2838446..2838457,
2859043..2859095

45 KLYKLERSYISKLTGLQLHFGKGRFGQVHKCEETATGLKLAAKIIKTR
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LFDRIIDESYNLT ELD TILFMKQICEGIRHMHQMYILHLDLKPENILCVNRDA

KQIKIDFGLARRYKLKVNFGTPEFLAPEVVNYDFVSFPTDMWSVGVIA YML
LSGLSPFLGDND AETLNNILACRWDLEDEEFQDISEEAK EFISKLLIKEKSWRI
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MDHKEWEVEEKERNQE (SEQ ID NO: 36)

MOOSE03368 ctg16775 599558..599733, 624104..624251, 628175..628228,
628324..628429, 629746..629811, 629902..629972, 631287..631343,
636534..636770, 642985..643104, 643578..643677, 645436..645545,
645693..645751, 652218..652288, 652509..652726, 662661..663016,
667436..667769

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VLRGKYRVPFYMSTDCESILRRFLVLNPAKRCTLEQIMKDKWINIGYEGEEL
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APLHPKRSPTSTGEAELKEERLPGRKASCSTAGSGRGLPPSSPMVSSAHNPN
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VCQLPRPGLRGVLFRRVAGTALAFRTLVTIRISNDLEL (SEQ ID NO: 42)

5 agtttgcgggcccggccgggaccccgacggccgtcggccgcctcctcctgtaccagcacctggcccagctgc
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35 MOOSE03372 ctg21fin5 107539..107634, 114972..115106, 117564..118777,
132517..132645, 134076..134256, 143434..143531, 152410..152623,
152852..153075, 153628..153751, 153861..153985, 154247..154417,
154592..154655, 158025..158141, 158641..158754, 166928..167047,
40 174177..174241, 196417..196459

MGRPGYGSRSHTPTASPASCAKRNASSLGPRLGGHTEQDSVSGKRK
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45 CHDHHIVHRDLKTENLLLDGNMDIKLAGTEDFGFGNFYKSGEPLSTWCGSP
PYAAPEVFEGKEYEGPQLDIWSLGVVLYVLVCGSLPFDGPNLPTLRQRVLE
GRFRIPFFMSQDCESLIRRMLVVDPAARRITIAQIRQHRWMRAEPLPGPACPA
FSAHSYTSNLGDYDEQALGIMQTLGVDRQRTVESLQNSSYNHFAAIYYLLL

ggacacacagagaaacacacacaacatgggtacacacaatacacaccacaaagacataaacctccccacacactcacat
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MOOSE03412 ctg13513 7184425..7185657, 7186318..7186470,
7187454..7187616, 7188719..7188850, 7190165..7190307, 7191013..7191144,
7196317..7196463

MVGKLSRRIYLSSARMVTTVPHVFSKLEMLSVSSSTHFTMRMRRRLM
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50)

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Table II

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68)

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70)

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MOOSE03305 ctg14493 3566412..3566482, 3568893..3569020,
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Table III

5	ctg14435_MOOSE03013.xml kinase family	AGC I Cyclic nucleotide regulated protein
	ctg17872_MOOSE03108.xml	AGC Other AGC-like kinases
	ctg15247_MOOSE03109.xml	AGC Other AGC-like kinases
	ctg17042_MOOSE03111.xml	AGC Other AGC-like kinases
10	ctg16439_MOOSE03177.xml close relatives family	CMGC I Cyclin-dependent kinases (CDKs) and
	ctg12913_MOOSE03184.xml close relatives family	CMGC I Cyclin-dependent kinases (CDKs) and
	ctg17937_MOOSE03219.xml	CMGC II ERK (MAP) kinase family
	ctg13541_MOOSE03228.xml	CMGC II ERK (MAP) kinase family
15	ctg15131_MOOSE03296.xml close relatives family	CaMK I Kinases regulated by Ca ²⁺ /CaM and
	ctg15131_MOOSE03301.xml close relatives family	CaMK I Kinases regulated by Ca ²⁺ /CaM and
20	ctg16704_MOOSE03304.xml close relatives family	CaMK I Kinases regulated by Ca ²⁺ /CaM and
	ctg19011_MOOSE03306.xml close relatives family	CaMK I Kinases regulated by Ca ²⁺ /CaM and
	ctg13286_MOOSE03309.xml close relatives family	CaMK I Kinases regulated by Ca ²⁺ /CaM and
25	ctg13538_MOOSE03312.xml close relatives family	CaMK I Kinases regulated by Ca ²⁺ /CaM and
	ctg595_MOOSE03313.xml close relatives family	CaMK I Kinases regulated by Ca ²⁺ /CaM and
30	ctg595_MOOSE03314.xml close relatives family	CaMK I Kinases regulated by Ca ²⁺ /CaM and
	ctg22fin3_MOOSE03316.xml close relatives family	CaMK I Kinases regulated by Ca ²⁺ /CaM and
	ctg14489_MOOSE03330.xml close relatives family	CaMK I Kinases regulated by Ca ²⁺ /CaM and
35	ctg15907_MOOSE03332.xml close relatives family	CaMK I Kinases regulated by Ca ²⁺ /CaM and
	ctg16586_MOOSE03340.xml close relatives family	CaMK I Kinases regulated by Ca ²⁺ /CaM and
40	ctg17207_MOOSE03350.xml close relatives family	CaMK I Kinases regulated by Ca ²⁺ /CaM and
	ctg16775_MOOSE03368.xml	CaMK II KIN1/SNF1/Nim1 family
	ctg21fin5_MOOSE03372.xml	CaMK II KIN1/SNF1/Nim1 family
	ctg13513_MOOSE03412.xml	OPK IV MEKK/STE11 family
	ctg15649_MOOSE03452.xml	OPK V NimA family
45	ctg15214_MOOSE03453.xml	OPK V NimA family
	ctg15214_MOOSE03455.xml	OPK V NimA family

ctg13079_MOOSE03475.xml OPK XI PSK/PTK “mixed lineage” leucine
 zipper domain family
ctg16734_MOOSE03605.xml PTK XI Eph/Elk/Eck orphan receptor family
ctg16574_MOOSE03608.xml PTK XI Eph/Elk/Eck orphan receptor family
5 ctg13657_MOOSE03639.xml PTK XVI Insulin receptor family
 MOOSE08717 OPK Other - Similar to Other Protein Kinases with no close
 relatives
 MOOSE08757 OPK XII - Casein Kinase I family
 MOOSE03397 OPK I - Polo family
10 MOOSE03609 PTK XI - Eph/Elk/Eck orphan receptor family
 MOOSE03184 CMGC I - Cyclin-dependent kinases (CDKs) and close
 relatives family
 MOOSE03305 CaMK I - Kinases regulated by Ca²⁺/CaM and close relatives
 family
15 MOOSE03302 CaMK I - Kinases regulated by Ca²⁺/CaM and close relatives
 family
 MOOSE03376 CaMK II - KIN1/SNF1/Nim1 family
 MOOSE03459 OPK VI - wee1/mik1 family
 MOOSE03283 CMGC Other - CMGK kinases
20

Table IV

KINASES

#####

Parkinson's Disease

Locus1 Marker:D1S231 Lod:5.11 CM_RANGE of one LOD drop:7

MOOSE08888 TK_XI_Eph/Elk/Eck_orphan_receptor_family
DISTANCE: -14.8 Mb

#####

COPD (Chronic Obstructive Pulmonary Disease)

Locus4 Marker:D19S884 Lod:2.9 CM_RANGE of one LOD drop:20

MOOSE08666 OPK_I_Polo_family
DISTANCE: -7.85 Mb

#####

Asthma

Locus2 Marker:D3S1546 Lod:3.4 CM_RANGE of one LOD drop:17

MOOSE08892 PTK_XI_Eph/Elk/Eck_orphan_receptor_family
DISTANCE: -7.75 Mb

#####

NIDDM (Non-insulin dep. Diabetes)

Locus1 Marker:D1S2884 Lod:3.4 CM_RANGE of one LOD drop: 16

MOOSE08580 CaMK_I_Kinases_regulated_by_Ca2+/CaM_and
_close_relatives_family
DISTANCE: 5.785 MbMOOSE08888 PTK_XI_Eph/Elk/Eck_orphan_receptor_family
DISTANCE: 12.53 Mb

#####

Migraine (Genomewide scan only)

Locus2 Marker:D2S2321 Lod:2.0 CM_RANGE of one LOD drop:5

MOOSE08409 CMGC_I_Cyclindependent_kinases_(CDKs)_

-93 -

and_close_relatives_family
DISTANCE: -5.66 Mb

#####

Bipolar (Genomewide scan only)

Locus1 Marker:D1S434 Lod:3.3 CM_RANGE of one LOD drop: 25

MOOSE08619 CaMK_I_Kinases_regulated_by_Ca2+/CaM_
and_close_relatives_family
DISTANCE: -4.43 Mb

#####

MI (Myocardial Infarction)

Locus4 Marker:D13S1250 Lod:3.2 CM_RANGE of one LOD drop: 5

MOOSE08757 OPK_XII_Casein_kinase_I_family
DISTANCE: 9.668 Mb

#####

Osteoarthritis

Locus2 Marker:D4S2999 Lod:3.8 CM_RANGE of one LOD drop:11

MOOSE08564 CaMK_I_Kinases_regulated_by_Ca2+/CaM_
and_close_relatives_family
DISTANCE: -3.47 Mb

#####

IBD (Inflammatory Bowel Disease)

Locus3 Marker:D13S1304 Lod:3.2 CM_RANGE of one LOD drop: 15

MOOSE08757 OPK_XII_Casein_kinase_I_family
DISTANCE: 11.55 Mb

CLAIMS

What is claimed is:

- 5 1. An isolated nucleic acid molecule comprising a protein kinase gene, wherein
 the protein kinase gene has a nucleotide sequence selected from the group of
 nucleic acid sequences as shown in Tables I and II, or the complements of
 the group of nucleic acid sequences as shown in Tables I and II.
- 10 2. A nucleic acid encoding a polypeptide, wherein the polypeptide has an amino
 acid sequence selected from the group consisting of the group of amino acid
 sequences as shown in Tables I and II.
- 15 3. An isolated nucleic acid molecule which hybridizes under high stringency
 conditions to a nucleotide sequence selected from the group of nucleic acid
 sequences as shown in Tables I and II, or the complements of the group of
 nucleic acid sequences as shown in Tables I and II.
- 20 4. An isolated nucleic molecule which hybridizes under high stringency
 conditions to a nucleotide sequence encoding an amino acid sequence
 selected from the group consisting of the group of amino acid sequences as
 shown in Tables I and II.
- 25 5. A method for assaying for the presence of a first nucleic acid molecule in a
 sample, comprising contacting said sample with a second nucleic acid
 molecule, where the second nucleic acid molecule comprises a nucleotide
 sequence selected from the group of nucleic acid sequences as shown in
 Tables I and II, and hybridizes to the first nucleic acid under high stringency
 conditions.
- 30 6. A vector comprising an isolated nucleic acid molecule selected from the group
 consisting of:
 - (a) the nucleic acid sequences as shown in Tables I and II;
 - (b) the complement of one of the nucleic acid sequences are shown in
35 Tables I and II; or

- (c) a nucleic acid encoding an amino acid molecule as shown in Tables I and II;
where the nucleic acid molecule is operably linked to a regulatory sequence.

- 5 7. A recombinant host cell comprising the vector of Claim 6.
8. A method for producing a polypeptide encoded by an isolated nucleic acid molecule, comprising culturing the recombinant host cell of Claim 7 under conditions suitable for expression of the nucleic acid molecule.
- 10 9. An isolated polypeptide encoded by the nucleotide sequence of the group of nucleic acid sequences as shown in Tables I and II, or the complements thereof.
- 15 10. The isolated polypeptide of Claim 9, wherein the polypeptide has an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.
- 20 11. An isolated polypeptide comprising an amino acid sequence, wherein the amino acid sequence is greater than about 95% identical to an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.
- 25 12. A fusion protein comprising an isolated polypeptide of Claim 2.
- 30 13. A fusion protein comprising an isolated polypeptide of Claim 11.
14. An antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of Claim 2, or to a fragment or variant of said amino acid sequence.
- 35 15. An antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of Claim 11, or to a fragment or variant of said amino acid sequence.

16. A method of assaying for the presence of a polypeptide encoded by an isolated nucleic acid molecule according to Claim 1 in a sample, the method comprising contacting the sample with an antibody which specifically binds to the encoded polypeptide.

5

17. A method of identifying an agent which alters the activity of a protein kinase, the method comprising:
- (a) contacting a polypeptide of Claim 9, or a derivative or fragment thereof, with an agent to be tested;
 - (b) assessing the level of activity of the polypeptide or derivative or fragment thereof; and
 - (c) comparing the level of activity with a level of activity of the polypeptide or active derivative or fragment thereof in the absence of the agent;
- wherein if the level of activity of the polypeptide or derivative or fragment thereof in the presence of the agent differs, by an amount that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters activity of a protein kinase.

10

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18. An agent which alters the activity of a protein kinase, identifiable according to the method of Claim 17.

19. The agent of Claim 18, where the agent is selected from the group consisting of: a protein kinase gene binding agent; a receptor; a peptidomimetic; a fusion protein; a prodrug; an antibody; and a ribozyme.

25

20. A method of altering activity of a polypeptide encoded by a protein kinase gene, comprising contacting the polypeptide with an agent of Claim 19.

21. A method of identifying an agent which alters interaction of the polypeptide of Claim 9 with a protein kinase gene binding agent, comprising:
- a) contacting the polypeptide or a derivative or fragment thereof, and the binding agent, with an agent to be tested;
 - b) assessing the interaction of the polypeptide or derivative or fragment thereof with the binding agent; and

30

35

- c) comparing the level of interaction with a level of interaction of the polypeptide or derivative or fragment thereof with the binding agent in the absence of the agent,

wherein if the level of interaction of the polypeptide or derivative or fragment thereof in the presence of the agent differs by an amount that is statistically significant, from the level of interaction in the absence of the agent, then the agent is an agent that alters interaction of the polypeptide with the binding agent.

22. An agent that alters interaction of a protein kinase gene polypeptide with a protein kinase gene binding agent, identifiable according to the method of Claim 21.

23. An agent which alters interaction of a protein kinase gene polypeptide with a protein kinase gene binding agent, selected from the group consisting of: a second protein kinase gene binding agent; a receptor; a peptidomimetic; a fusion protein; a prodrug; an antibody; and a ribozyme.

24. A method of altering interaction of a protein kinase gene polypeptide with a protein kinase gene binding agent, comprising contacting the protein kinase gene polypeptide and/or the protein kinase gene binding agent with an agent of Claim 23.

25. A method of identifying an agent that alters expression of a protein kinase gene, comprising the steps of:

- a) contacting a solution containing a nucleic acid comprising the promoter region of the protein kinase gene operably linked to a reporter gene with an agent to be tested;
- b) assessing the level of expression of the reporter gene; and
- c) comparing the level of expression with a level of expression of the reporter gene in the absence of the agent,

wherein if the level of expression of the reporter gene in the presence of the agent differs, by an amount that is statistically significant, from the level of expression in the absence of the agent, then the agent is an agent that alters expression of the protein kinase gene.

26. An agent that alters expression of the protein kinase gene, identifiable according to the method of Claim 25.
27. A method of identifying an agent that alters expression of a protein kinase gene, comprising the steps of:
- a) contacting a solution containing a nucleic acid of Claim 1 or a derivative or fragment thereof with an agent to be tested;
 - b) assessing expression of the nucleic acid, derivative or fragment; and
 - c) comparing expression with expression of the nucleic acid, derivative or fragment in the absence of the agent,
- wherein if expression of the nucleotide, derivative or fragment in the presence of the agent differs, by an amount that is statistically significant, from the expression in the absence of the agent, then the agent is an agent that alters expression of the protein kinase gene.
28. The method of Claim 27, wherein the expression of the nucleotide, derivative or fragment in the presence of the agent comprises expression of one or more splicing variant(s) that differ in kind or in quantity from the expression of one or more splicing variant(s) the absence of the agent.
29. An agent that alters expression of a protein kinase gene, identifiable according to the method of Claim 27.
30. An agent that alters expression of a protein kinase gene, selected from the group consisting of: antisense nucleic acid to a protein kinase gene; a protein kinase gene polypeptide; a protein kinase gene receptor; a protein kinase gene binding agent; a peptidomimetic; a fusion protein; a prodrug thereof; an antibody; and a ribozyme.
31. A method of altering expression of a protein kinase gene, comprising contacting a cell containing a protein kinase gene with an agent of Claim 30.
32. A method of identifying a polypeptide which interacts with a protein kinase gene polypeptide, comprising employing a yeast two-hybrid system using a first vector which comprises a nucleic acid encoding a DNA binding domain and a protein kinase gene polypeptide, splicing variant, or a fragment or

derivative thereof, and a second vector which comprises a nucleic acid encoding a transcription activation domain and a nucleic acid encoding a test polypeptide, wherein if transcriptional activation occurs in the yeast two-hybrid system, the test polypeptide is a polypeptide which interacts with a protein kinase polypeptide.

33. A protein kinase gene therapeutic agent selected from the group consisting of: a protein kinase gene or fragment or derivative thereof; a polypeptide encoded by a protein kinase gene; a receptor; a protein kinase gene binding agent; a peptidomimetic; a fusion protein; a prodrug; an antibody; an agent that alters protein kinase gene expression; an agent that alters activity of a polypeptide encoded by a protein kinase gene; an agent that alters posttranscriptional processing of a polypeptide encoded by a protein kinase gene; an agent that alters interaction of a protein kinase gene with a protein kinase gene binding agent; an agent that alters transcription of splicing variants encoded by a protein kinase gene; and a ribozyme.
34. A pharmaceutical composition comprising a protein kinase gene therapeutic agent of Claim 33.
35. The pharmaceutical composition of Claim 34, wherein the protein kinase gene therapeutic agent is an isolated nucleic acid molecule comprising a protein kinase gene or fragment or derivative thereof.
36. The pharmaceutical composition of Claim 34, wherein the protein kinase gene therapeutic agent is a polypeptide encoded by the protein kinase gene.
37. A method of treating a disease or condition associated with a protein kinase in an individual, comprising administering a protein kinase gene therapeutic agent to the individual, in a therapeutically effective amount.
38. The method of Claim 37, wherein the protein kinase gene therapeutic agent is a protein kinase gene agonist.
39. The method of Claim 38 wherein the protein kinase gene therapeutic agent is a protein kinase gene antagonist.

- 5
40. A transgenic animal comprising a nucleic acid selected from the group consisting of: an exogenous protein kinase gene and a nucleic acid encoding a protein kinase gene polypeptide.
- 10
41. A method for assaying a sample for the presence of a protein kinase gene nucleic acid, comprising:
- 15
- a) contacting said sample with a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said protein kinase gene nucleic acid under conditions appropriate for hybridization, and
- b) assessing whether hybridization has occurred between a protein kinase gene nucleic acid and said nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said protein kinase gene nucleic acid; wherein if hybridization has occurred, a protein kinase gene is present in the nucleic acid.
- 20
42. The method of Claim 41, wherein said nucleic acid comprising a contiguous nucleotide sequence is completely complementary to a part of the sequence of said protein kinase gene nucleic acid.
- 25
43. The method of Claim 41, comprising amplification of at least part of said protein kinase gene nucleic acid.
- 30
44. The method of Claim 41, wherein said contiguous nucleotide sequence is 100 or fewer nucleotides in length and is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or c) capable of selectively hybridizing to said protein kinase gene nucleic acid.
- 35
45. A reagent for assaying a sample for the presence of a protein kinase gene nucleic acid, said reagent comprising a nucleic acid comprising a contiguous

nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said protein kinase gene nucleic acid.

5 46. The reagent of Claim 45, wherein the nucleic acid comprises a contiguous nucleotide sequence that is completely complementary to a part of the nucleotide sequence of said protein kinase gene nucleic acid.

47. A reagent kit for assaying a sample for the presence of a protein kinase gene nucleic acid, comprising in separate containers:

- 10 a) one or more labeled nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said protein kinase gene nucleic acid, and
b) reagents for detection of said label.

15 48. The reagent kit of Claim 47, wherein the labeled nucleic acid comprises a contiguous nucleotide sequences which is completely complementary to a part of the nucleotide sequence of said protein kinase gene nucleic acid.

20 49. A reagent kit for assaying a sample for the presence of a protein kinase gene nucleic acid, comprising one or more nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said protein kinase gene nucleic acid, and which is capable of acting as a primer for said protein kinase gene nucleic acid when maintained under conditions for primer extension.

25 50. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II;
30 b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or c) capable of selectively hybridizing to said protein kinase gene nucleic acid, for assaying a sample for the presence of a protein kinase gene nucleic acid.

35 51. The use of a first nucleic acid which is 100 or fewer nucleotides in length and which is either:

- 5
- a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II;
 - b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or
 - c) capable of selectively hybridizing to said protein kinase gene nucleic acid;

for assaying a sample for the presence of a protein kinase gene nucleic acid that has at least one nucleotide difference from the first nucleic acid.

10 52. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either:

- 15
- a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II;
 - b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or
 - c) capable of selectively hybridizing to said protein kinase gene nucleic acid;

20 for diagnosing a susceptibility to a disease or condition associated with a protein kinase.

1/155

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Martinez, Roger Alfonso Moraga
Sigurdsson, Gunnar Thor

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2/155

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Val	Cys	Leu	Ala	Cys	Lys	Val	Asp	Thr	His	Ala	Leu	Tyr	Ala	Met	Lys	
	130					135					140					
acc	cta	agg	aaa	aag	gat	gtc	ctg	aac	cgg	aat	cag	gtg	gcc	cac	gtc	480
Thr	Leu	Arg	Lys	Lys	Asp	Val	Leu	Asn	Arg	Asn	Gln	Val	Ala	His	Val	
145					150					155					160	
aag	gcc	gag	agg	gac	atc	ctg	gcc	gag	gca	gac	aat	gag	tgg	gtg	gtc	528
Lys	Ala	Glu	Arg	Asp	Ile	Leu	Ala	Glu	Ala	Asp	Asn	Glu	Trp	Val	Val	
				165					170					175		
aaa	ctc	tac	tac	tcc	ttc	caa	gac	aaa	gac	agc	ctg	tac	ttt	gtg	atg	576
Lys	Leu	Tyr	Tyr	Ser	Phe	Gln	Asp	Lys	Asp	Ser	Leu	Tyr	Phe	Val	Met	
			180					185					190			
gac	tac	atc	cct	ggg	ggg	gac	atg	atg	agc	ctg	ctg	atc	cgg	atg	gag	624
Asp	Tyr	Ile	Pro	Gly	Gly	Asp	Met	Met	Ser	Leu	Leu	Ile	Arg	Met	Glu	
		195					200					205				
gtc	ttc	cct	gag	cac	ctg	gcc	cgg	ttc	tac	atc	gca	gag	ctg	act	ttg	672
Val	Phe	Pro	Glu	His	Leu	Ala	Arg	Phe	Tyr	Ile	Ala	Glu	Leu	Thr	Leu	
	210					215					220					
gcc	att	gag	agt	gtc	cac	aag	atg	ggc	ttc	atc	cac	cga	gac	atc	aag	720
Ala	Ile	Glu	Ser	Val	His	Lys	Met	Gly	Phe	Ile	His	Arg	Asp	Ile	Lys	
225					230				235						240	
cct	gat	aac	att	ttg	ata	gat	ctg	gat	ggg	cac	att	aaa	ctc	aca	gat	768
Pro	Asp	Asn	Ile	Leu	Ile	Asp	Leu	Asp	Gly	His	Ile	Lys	Leu	Thr	Asp	
				245					250					255		
ttc	ggc	ctc	tgc	act	ggg	ttc	agg	tgc	ctg	gca	cat	tca	ctg	gtg	ggg	816
Phe	Gly	Leu	Cys	Thr	Gly	Phe	Arg	Cys	Leu	Ala	His	Ser	Leu	Val	Gly	
			260					265					270			
act	cca	aac	tac	atc	gca	ccc	gag	gtg	ctc	ctc	cgc	aaa	ggg	tac	act	864
Thr	Pro	Asn	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Leu	Arg	Lys	Gly	Tyr	Thr	
		275					280					285				
caa	ctc	tgt	gac	tgg	tgg	agt	ggt	gga	gtg	att	ctc	ttc	gag	atg	ctg	912
Gln	Leu	Cys	Asp	Trp	Trp	Ser	Val	Gly	Val	Ile	Leu	Phe	Glu	Met	Leu	
	290					295					300					
gtg	ggg	cag	ccg	ccc	ttt	ttg	gca	cct	act	ccc	aca	gaa	acc	cag	ctg	960
Val	Gly	Gln	Pro	Pro	Phe	Leu	Ala	Pro	Thr	Pro	Thr	Glu	Thr	Gln	Leu	
305					310					315					320	
aag	gta	atc	cac	tgt	gcc	tgg	cct	cgg	gac	ttc	ttc	cct	gag	gcc	agg	1008
Lys	Val	Ile	His	Cys	Ala	Trp	Pro	Arg	Asp	Phe	Phe	Pro	Glu	Ala	Arg	
				325					330					335		
gac	ctc	atc	acc	aag	ctg	tgc	tgc	tcc	gca	gac	cac	cgc	ctg	ggg	cgg	1056
Asp	Leu	Ile	Thr	Lys	Leu	Cys	Cys	Ser	Ala	Asp	His	Arg	Leu	Gly	Arg	
			340					345					350			

3/155

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aat ggg gcc gat gac ctg aag gcc cac ccc ttc ttc agc gcc att gac 1104
Asn Gly Ala Asp Asp Leu Lys Ala His Pro Phe Phe Ser Ala Ile Asp
      355      360      365

ttc tcc agt gac atc cgg aag cag cca gcc ccc tac gtt ccc acc atc 1152
Phe Ser Ser Asp Ile Arg Lys Gln Pro Ala Pro Tyr Val Pro Thr Ile
      370      375      380

agc cac ccc atg gac acc tcg aat ttc gac ccc gta gat gaa gaa agc 1200
Ser His Pro Met Asp Thr Ser Asn Phe Asp Pro Val Asp Glu Glu Ser
385      390      395      400

cct tgg aac gat gcc agc gaa ggt agc acc aag gcc tgg gac aca 1245
Pro Trp Asn Asp Ala Ser Glu Gly Ser Thr Lys Ala Trp Asp Thr
      405      410      415

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<210> 2
 <211> 415
 <212> PRT
 <213> Homo sapiens

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Leu Ser Gln Asn Asn Ser Ser Asn Lys Asn Asn Lys Thr Ser Asn Lys
 1      5      10      15
Asn Ala His Phe Gln Val Arg Pro Thr Glu Ser Glu Thr Leu Gly Glu
      20      25      30
Ala Gln Gln Ser Gln Phe Gly Arg Ala Arg Gln Glu Asp His Leu Ser
      35      40      45
Pro Gly Val Pro Asp Gln Pro Gly Gln His Ser His Ser Gly Trp Gly
50      55      60
Met Pro Ser Ala Pro Ala Leu Gly Gly Asp Ser Ala Cys Phe Ala Asp
65      70      75      80
Cys Pro Thr Ser Gln Thr Glu Gln Glu Gln Met Arg Lys Ile Leu Tyr
      85      90      95
Gln Lys Glu Ser Asn Tyr Asn Arg Leu Lys Arg Ala Lys Met Asp Lys
100      105      110
Ser Met Phe Val Lys Ile Lys Thr Leu Gly Ile Gly Ala Phe Gly Glu
115      120      125
Val Cys Leu Ala Cys Lys Val Asp Thr His Ala Leu Tyr Ala Met Lys
130      135      140
Thr Leu Arg Lys Lys Asp Val Leu Asn Arg Asn Gln Val Ala His Val
145      150      155      160
Lys Ala Glu Arg Asp Ile Leu Ala Glu Ala Asp Asn Glu Trp Val Val
165      170      175
Lys Leu Tyr Tyr Ser Phe Gln Asp Lys Asp Ser Leu Tyr Phe Val Met
180      185      190
Asp Tyr Ile Pro Gly Gly Asp Met Met Ser Leu Leu Ile Arg Met Glu
195      200      205
Val Phe Pro Glu His Leu Ala Arg Phe Tyr Ile Ala Glu Leu Thr Leu
210      215      220
Ala Ile Glu Ser Val His Lys Met Gly Phe Ile His Arg Asp Ile Lys
225      230      235      240
Pro Asp Asn Ile Leu Ile Asp Leu Asp Gly His Ile Lys Leu Thr Asp
245      250      255
Phe Gly Leu Cys Thr Gly Phe Arg Cys Leu Ala His Ser Leu Val Gly
260      265      270
Thr Pro Asn Tyr Ile Ala Pro Glu Val Leu Leu Arg Lys Gly Tyr Thr
275      280      285
Gln Leu Cys Asp Trp Trp Ser Val Gly Val Ile Leu Phe Glu Met Leu
290      295      300

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4/155

Val	Gly	Gln	Pro	Pro	Phe	Leu	Ala	Pro	Thr	Pro	Thr	Glu	Thr	Gln	Leu
305					310					315					320
Lys	Val	Ile	His	Cys	Ala	Trp	Pro	Arg	Asp	Phe	Phe	Pro	Glu	Ala	Arg
				325					330					335	
Asp	Leu	Ile	Thr	Lys	Leu	Cys	Cys	Ser	Ala	Asp	His	Arg	Leu	Gly	Arg
			340					345					350		
Asn	Gly	Ala	Asp	Asp	Leu	Lys	Ala	His	Pro	Phe	Phe	Ser	Ala	Ile	Asp
		355					360					365			
Phe	Ser	Ser	Asp	Ile	Arg	Lys	Gln	Pro	Ala	Pro	Tyr	Val	Pro	Thr	Ile
	370					375					380				
Ser	His	Pro	Met	Asp	Thr	Ser	Asn	Phe	Asp	Pro	Val	Asp	Glu	Glu	Ser
385					390					395					400
Pro	Trp	Asn	Asp	Ala	Ser	Glu	Gly	Ser	Thr	Lys	Ala	Trp	Asp	Thr	
				405					410					415	

<210> 3
 <211> 3153
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(3153)
 <223> MOOSE03108

<400> 3																
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Leu	Glu	Gly	Glu	Val	Glu	Thr	Arg	His	Ser	Glu	Val	Thr	Ala	Ser	Cys	
1				5					10					15		
gtg	ctc	tgt	cca	cga	gcc	agg	cct	tta	cct	gcc	cca	ggg	gta	ggg	cgt	96
Val	Leu	Cys	Pro	Arg	Ala	Arg	Pro	Leu	Pro	Ala	Pro	Gly	Val	Gly	Arg	
			20					25					30			
tct	agg	ggc	ttg	ggg	gct	gat	caa	gga	aat	aga	tgc	cca	ccc	agt	ggg	144
Ser	Arg	Gly	Leu	Gly	Ala	Asp	Gln	Gly	Asn	Arg	Cys	Pro	Pro	Ser	Gly	
		35					40					45				
agt	agc	acg	cac	ata	agc	ctt	ttg	gag	gct	gag	gtt	cca	gga	gtc	acc	192
Ser	Ser	Thr	His	Ile	Ser	Leu	Leu	Glu	Ala	Glu	Val	Pro	Gly	Val	Thr	
		50				55					60					
atc	aag	agg	gag	agg	ccg	gca	agg	gaa	ctc	ccc	ggg	cag	agg	ggg	atc	240
Ile	Lys	Arg	Glu	Arg	Pro	Ala	Arg	Glu	Leu	Pro	Gly	Gln	Arg	Gly	Ile	
	65				70				75					80		
aga	gag	ggg	gct	tac	atg	gcc	gtc	tac	ctg	gtg	cgg	cac	cgt	gac	aca	288
Arg	Glu	Gly	Ala	Tyr	Met	Ala	Val	Tyr	Leu	Val	Arg	His	Arg	Asp	Thr	
				85					90					95		
cgg	cag	cgc	ttt	gcc	atc	aag	aag	atc	aac	aaa	cag	aac	ttg	atc	ctg	336
Arg	Gln	Arg	Phe	Ala	Ile	Lys	Lys	Ile	Asn	Lys	Gln	Asn	Leu	Ile	Leu	
			100					105					110			
cgt	aac	cag	atc	cag	cag	gtc	ttt	gtg	gag	cgt	gac	att	ctc	acc	ttt	384
Arg	Asn	Gln	Ile	Gln	Gln	Val	Phe	Val	Glu	Arg	Asp	Ile	Leu	Thr	Phe	
		115					120					125				
gcc	gag	aac	ccc	ttt	gtg	gtc	agc	atg	ttc	tgc	tcc	ttt	gag	acc	cgg	432
Ala	Glu	Asn	Pro	Phe	Val	Val	Ser	Met	Phe	Cys	Ser	Phe	Glu	Thr	Arg	
	130						135				140					

5/155

cgc	cac	cta	tgt	atg	gtc	atg	gaa	tac	gtg	gaa	ggc	ggc	gac	tgc	gcc	480
Arg	His	Leu	Cys	Met	Val	Met	Glu	Tyr	Val	Glu	Gly	Gly	Asp	Cys	Ala	
145					150					155					160	
acg	ctc	ctg	aag	aac	atg	ggc	ccg	ctg	ccc	gtg	gac	atg	gcc	cgc	ctg	528
Thr	Leu	Leu	Lys	Asn	Met	Gly	Pro	Leu	Pro	Val	Asp	Met	Ala	Arg	Leu	
				165					170					175		
tac	ttc	gcc	gag	acg	gtg	ttg	gcg	ctg	gag	tac	ctg	cat	aac	tat	ggc	576
Tyr	Phe	Ala	Glu	Thr	Val	Leu	Ala	Leu	Glu	Tyr	Leu	His	Asn	Tyr	Gly	
			180					185					190			
atc	gtg	cac	cgt	gac	ctc	aaa	cca	gac	aat	ctg	ctc	atc	acc	tcg	ctt	624
Ile	Val	His	Arg	Asp	Leu	Lys	Pro	Asp	Asn	Leu	Leu	Ile	Thr	Ser	Leu	
		195					200					205				
ggc	cac	atc	aag	ctc	acg	gac	ttc	ggc	ctg	tcc	aag	atc	ggc	ctc	atg	672
Gly	His	Ile	Lys	Leu	Thr	Asp	Phe	Gly	Leu	Ser	Lys	Ile	Gly	Leu	Met	
	210					215					220					
agc	atg	gcc	acc	aac	ctc	tat	gag	ggc	cac	atc	gag	aag	gac	gcc	cga	720
Ser	Met	Ala	Thr	Asn	Leu	Tyr	Glu	Gly	His	Ile	Glu	Lys	Asp	Ala	Arg	
	225				230					235					240	
gag	ttc	atc	gac	aag	cag	gtg	tgt	ggg	acg	ccg	gag	tac	ata	gcc	ccc	768
Glu	Phe	Ile	Asp	Lys	Gln	Val	Cys	Gly	Thr	Pro	Glu	Tyr	Ile	Ala	Pro	
			245					250						255		
gag	gtg	atc	ttc	cgc	cag	ggc	tat	ggg	aag	cca	gtg	gac	tgg	tgg	gcc	816
Glu	Val	Ile	Phe	Arg	Gln	Gly	Tyr	Gly	Lys	Pro	Val	Asp	Trp	Trp	Ala	
		260					265						270			
atg	ggc	gtc	gtc	ctc	tat	gag	ttt	ctg	gtg	ggc	tgc	gtg	cct	ttc	ttt	864
Met	Gly	Val	Val	Leu	Tyr	Glu	Phe	Leu	Val	Gly	Cys	Val	Pro	Phe	Phe	
		275				280						285				
gga	gat	acc	ccc	gag	gaa	ctc	ttc	ggg	cag	gtg	gtc	agc	gat	gag	atc	912
Gly	Asp	Thr	Pro	Glu	Glu	Leu	Phe	Gly	Gln	Val	Val	Ser	Asp	Glu	Ile	
	290					295					300					
atg	tgg	cca	gag	gga	gat	gag	gcc	ctt	cca	gca	gac	gcc	cag	gac	ctc	960
Met	Trp	Pro	Glu	Gly	Asp	Glu	Ala	Leu	Pro	Ala	Asp	Ala	Gln	Asp	Leu	
	305				310					315					320	
atc	acc	agg	ttg	ctc	cgg	cag	agc	ccg	ctg	gac	cgt	ctg	ggc	act	ggg	1008
Ile	Thr	Arg	Leu	Leu	Arg	Gln	Ser	Pro	Leu	Asp	Arg	Leu	Gly	Thr	Gly	
				325					330					335		
ggc	acc	cac	gaa	gtg	aag	cag	cac	ccc	ttt	ttc	ctg	gcc	ctg	gac	tgg	1056
Gly	Thr	His	Glu	Val	Lys	Gln	His	Pro	Phe	Phe	Leu	Ala	Leu	Asp	Trp	
			340					345					350			
gca	ggg	ctt	ctc	cga	cac	aaa	gcc	gag	ttc	gtg	ccc	cag	ctc	gaa	gct	1104
Ala	Gly	Leu	Leu	Arg	His	Lys	Ala	Glu	Phe	Val	Pro	Gln	Leu	Glu	Ala	
		355					360					365				
gag	gat	gat	acc	agc	tac	ttt	gac	aca	cgt	tcg	gaa	cgt	tac	cgc	cat	1152
Glu	Asp	Asp	Thr	Ser	Tyr	Phe	Asp	Thr	Arg	Ser	Glu	Arg	Tyr	Arg	His	
	370					375					380					

6/155

ctg ggc tcc gag gac gac gag acc aat gat gaa gaa tcg tcc aca gag	1200
Leu Gly Ser Glu Asp Asp Glu Thr Asn Asp Glu Glu Ser Ser Thr Glu	
385 390 395 400	
atc ccc cag ttc tcc tcc tgc tcc cac cgg ttc agc aag gtc tac agc	1248
Ile Pro Gln Phe Ser Ser Cys Ser His Arg Phe Ser Lys Val Tyr Ser	
405 410 415	
agc tct gag ttc ctg gcc gtc cag ccc act cct acc ttc gct gaa agg	1296
Ser Ser Glu Phe Leu Ala Val Gln Pro Thr Pro Thr Phe Ala Glu Arg	
420 425 430	
agc ttc agt gaa gac cgg gag gag gga gcc tcc tcc agc ggt ggc agt	1344
Ser Phe Ser Glu Asp Arg Glu Glu Gly Ala Ser Ser Ser Gly Gly Ser	
435 440 445	
ggt ggc ggc agt ggg ggc cgc gtg ccc aag tca gcc tct gtc tct gcc	1392
Gly Gly Gly Ser Gly Gly Arg Val Pro Lys Ser Ala Ser Val Ser Ala	
450 455 460	
ctg tcc ctc atc atc acg gca gat gat ggc agc ggc ggc ccc ctc atg	1440
Leu Ser Leu Ile Ile Thr Ala Asp Asp Gly Ser Gly Gly Pro Leu Met	
465 470 475 480	
agc ccc ctt tcc ccg cgc tct ctg tcc tcg aac ccg tcg tcc cgt gac	1488
Ser Pro Leu Ser Pro Arg Ser Leu Ser Ser Asn Pro Ser Ser Arg Asp	
485 490 495	
tct tcg ccg agc cga gac ccg tcc ccc gtg tgt ggc agc ctg cgg ccc	1536
Ser Ser Pro Ser Arg Asp Pro Ser Pro Val Cys Gly Ser Leu Arg Pro	
500 505 510	
ccc atc gtt atc cac agc tct ggc aag aag tac ggc ttc agc ctg cgg	1584
Pro Ile Val Ile His Ser Ser Gly Lys Lys Tyr Gly Phe Ser Leu Arg	
515 520 525	
gcg atc cgc gtc tac atg ggt gat agc gac gtc tac act gtg cac cac	1632
Ala Ile Arg Val Tyr Met Gly Asp Ser Asp Val Tyr Thr Val His His	
530 535 540	
gtc gtc tgg agt gtg gag gac gga agc ccc gcc cag gag gcg ggc ctg	1680
Val Val Trp Ser Val Glu Asp Gly Ser Pro Ala Gln Glu Ala Gly Leu	
545 550 555 560	
cgg gct ggg gac ctc atc acc cac atc aac ggg gag tca gtg ctg ggg	1728
Arg Ala Gly Asp Leu Ile Thr His Ile Asn Gly Glu Ser Val Leu Gly	
565 570 575	
ctg gtg cac atg gac gtc gtg gag ctg ctg ctg aag agc ggc aac aag	1776
Leu Val His Met Asp Val Val Glu Leu Leu Leu Lys Ser Gly Asn Lys	
580 585 590	
ata tcc ctg cgg acc aca gcc ctg gag aac acc tcc atc aag gtg ggc	1824
Ile Ser Leu Arg Thr Thr Ala Leu Glu Asn Thr Ser Ile Lys Val Gly	
595 600 605	
ccc gcc cgg aag aat gtg gcc aag ggc cgc atg gca cgc agg agc aag	1872
Pro Ala Arg Lys Asn Val Ala Lys Gly Arg Met Ala Arg Arg Ser Lys	
610 615 620	

7/155

agg Arg 625	agc Ser	cgt Arg	cgg Arg	cgg Arg	gag Glu 630	acc Thr	cag Gln	gat Asp	cgg Arg	cgg Arg 635	aag Lys	tca Ser	ctt Leu	ttc Phe	aag Lys 640	1920
aag Lys	atc Ile	tcc Ser	aag Lys	cag Gln 645	acc Thr	tcc Ser	gtg Val	ctg Leu	cac His 650	acc Thr	agc Ser	cgc Arg	agc Ser	ttc Phe 655	tcc Ser	1968
tcc Ser	gga Gly	ctc Leu	cac His 660	cac His	tca Ser	ctg Leu	tca Ser	tcc Ser 665	agt Ser	gag Glu	agc Ser	ctc Leu	ccc Pro 670	ggc Gly	tcg Ser	2016
ccc Pro	acc Thr	cac His 675	agc Ser	ctc Leu	tcc Ser	ccc Pro	agc Ser 680	ccc Pro	acc Thr	act Thr	ccc Pro	tgc Cys 685	cga Arg	agc Ser	cca Pro	2064
gcc Ala	cct Pro	gat Asp	gtc Val	cca Pro	gca Ala	gat Asp 695	acc Thr	act Thr	gca Ala	tcc Ser	cca Pro	ccc Pro	agc Ser	gca Ala	tcc Ser	2112
ccg Pro 705	agc Ser	tcc Ser	agc Ser	agc Ser	ccc Pro 710	gcc Ala	tcc Ser	cca Pro	gct Ala	gct Ala 715	gct Ala	ggc Gly	cac His	acc Thr	cgc Arg 720	2160
ccc Pro	agc Ser	tcc Ser	ctg Leu	cac His 725	ggc Gly	ctg Leu	gct Ala	gcc Ala	aag Lys 730	ctt Leu	ggg Gly	cca Pro	ccc Pro	cgc Arg 735	ccc Pro	2208
aag Lys	act Thr	ggc Gly	cgc Arg	cgc Arg	aag Lys	tcc Ser	acc Thr	agc Ser	agc Ser	atc Ile	ccg Pro	ccc Pro	tcc Ser	ccg Pro	ctg Leu	2256
gcc Ala	tgc Cys	ccg Pro 755	ccc Pro	atc Ile	tcc Ser	gcg Ala	ccc Pro 760	cca Pro	ccc Pro	cgc Arg	tcg Ser	ccc Pro 765	tcg Ser	ccc Pro	ctg Leu	2304
ccc Pro 770	ggg Gly	cac His	ccg Pro	ccc Pro	gca Ala	cct Pro 775	gcc Ala	cga Arg	tcc Ser	ccg Pro	cgg Arg 780	ctg Leu	cgc Arg	cgg Arg	ggc Gly	2352
cag Gln 785	tca Ser	gct Ala	gac Asp	aag Lys	ctg Leu 790	ggc Gly	aca Thr	ggg Gly	gag Glu	cgg Arg 795	ctg Leu	gat Asp	ggg Gly	gag Glu	gcg Ala 800	2400
ggg Gly	cgg Arg	cgc Arg	act Thr	cgt Arg 805	ggg Gly	cca Pro	gag Glu	gcc Ala	gag Glu 810	ctc Leu	gtg Val	gtc Val	atg Met	cgg Arg 815	cgg Arg	2448
ctg Leu	cac His	ctg Leu	tcc Ser 820	gag Glu	cgc Arg	cga Arg	gac Asp	tcc Ser 825	ttc Phe	aag Lys	aag Lys	cag Gln	gag Glu	gcc Ala	gtg Val	2496
cag Gln	gag Glu	gtt Val 835	agc Ser	ttc Phe	gat Asp	gag Glu	ccg Pro 840	cag Gln	gag Glu	gag Glu	gcc Ala	act Thr 845	ggg Gly	ctg Leu	ccc Pro	2544
acc Thr 850	tca Ser	gtg Val	cca Pro	cag Gln	atc Ile	gcc Ala 855	gtg Val	gag Glu	ggc Gly	gag Glu	gaa Glu 860	gcc Ala	act Thr	gag Glu	gca Ala	2592

8/155

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cag aac cga cag ctg ccc tcc acc acg cgt ggc ctc atg gcg tct ttg 2640
Gln Asn Arg Gln Leu Pro Ser Thr Thr Arg Gly Leu Met Ala Ser Leu
865                               870                               875                               880

act tgg act cct gtt tac cac cct ccc cat cac acc cag aat cca cac 2688
Thr Trp Thr Pro Val Tyr His Pro Pro His His Thr Gln Asn Pro His
                               885                               890                               895

ccc cac tgc gac gtc att gtc cct tca gcc ctc ccc aac cct ggg gcc 2736
Pro His Cys Asp Val Ile Val Pro Ser Ala Leu Pro Asn Pro Gly Ala
                               900                               905                               910

tca ctg tcc ttg tct tgc ctg cag ctc tac gcc cca ggg ctg tcg cca 2784
Ser Leu                               915                               920                               925

gac act atc atg gag tgt gca atg ggg gac cgc ggc atg cag ctc atg 2832
Asp Thr Ile Met Glu Cys Ala Met Gly Asp Arg Gly Met Gln Leu Met
930                               935                               940

cac gcc aac gcc cag cgg aca gat gct ctc cag cca cca cac gaa gag 2880
His Ala Asn Ala Gln Arg Thr Asp Ala Leu Gln Pro Pro His Glu Glu
945                               950                               955                               960

tct cct gcc tca gcc tcc cga gta gct ggg act aca agc ggg tgc tac 2928
Ser Pro Ala Ser Ala Ser Arg Val Ala Gly Thr Thr Ser Gly Cys Tyr
                               965                               970                               975

cac acc tgg cta ttt ttt ttt ttt tat gag ccg aga tcg cgc cac tgc 2976
His Thr Trp Leu Phe Phe Phe Phe Tyr Glu Pro Arg Ser Arg His Cys
980                               985                               990

act cca gcc tgg gcg aca gtt cga gac tcc gtc tca aac aaa caa aaa 3024
Thr Pro Ala Trp Ala Thr Val Arg Asp Ser Val Ser Asn Lys Gln Lys
995                               1000                               1005

gac cca acc ctt ctc tgc tca ttc ggt cca agt atg acc ggg tct gag 3072
Asp Pro Thr Leu Leu Cys Ser Phe Gly Pro Ser Met Thr Gly Ser Glu
1010                               1015                               1020

ttg ggt ctg atc acg tcg aat tgg act tgg tca cga aga gtt tgt tcg 3120
Leu Gly Leu Ile Thr                               1030                               1035                               1040
1025

atg acc tca gcc cgt ccc act ctg ggc ctc aca 3153
Met Thr Ser Ala Arg Pro Thr Leu Gly Leu Thr
                               1045                               1050

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<210> 4

<211> 1051

<212> PRT

<213> Homo sapiens

<400> 4

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Leu Glu Gly Glu Val Glu Thr Arg His Ser Glu Val Thr Ala Ser Cys
 1          5          10          15
Val Leu Cys Pro Arg Ala Arg Pro Leu Pro Ala Pro Gly Val Gly Arg
 20          25          30
Ser Arg Gly Leu Gly Ala Asp Gln Gly Asn Arg Cys Pro Pro Ser Gly
 35          40          45

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9/155

Ser	Ser	Thr	His	Ile	Ser	Leu	Leu	Glu	Ala	Glu	Val	Pro	Gly	Val	Thr
	50					55					60				
Ile	Lys	Arg	Glu	Arg	Pro	Ala	Arg	Glu	Leu	Pro	Gly	Gln	Arg	Gly	Ile
65					70					75					80
Arg	Glu	Gly	Ala	Tyr	Met	Ala	Val	Tyr	Leu	Val	Arg	His	Arg	Asp	Thr
				85					90					95	
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Ala	Glu	Asn	Pro	Phe	Val	Val	Ser	Met	Phe	Cys	Ser	Phe	Glu	Thr	Arg
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Arg	His	Leu	Cys	Met	Val	Met	Glu	Tyr	Val	Glu	Gly	Gly	Asp	Cys	Ala
145					150					155					160
Thr	Leu	Leu	Lys	Asn	Met	Gly	Pro	Leu	Pro	Val	Asp	Met	Ala	Arg	Leu
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Tyr	Phe	Ala	Glu	Thr	Val	Leu	Ala	Leu	Glu	Tyr	Leu	His	Asn	Tyr	Gly
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Glu	Phe	Ile	Asp	Lys	Gln	Val	Cys	Gly	Thr	Pro	Glu	Tyr	Ile	Ala	Pro
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Glu	Val	Ile	Phe	Arg	Gln	Gly	Tyr	Gly	Lys	Pro	Val	Asp	Trp	Trp	Ala
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Glu	Asp	Asp	Thr	Ser	Tyr	Phe	Asp	Thr	Arg	Ser	Glu	Arg	Tyr	Arg	His
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Leu	Gly	Ser	Glu	Asp	Asp	Glu	Thr	Asn	Asp	Glu	Glu	Ser	Ser	Thr	Glu
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Ile	Pro	Gln	Phe	Ser	Ser	Cys	Ser	His	Arg	Phe	Ser	Lys	Val	Tyr	Ser
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Ser	Phe	Ser	Glu	Asp	Arg	Glu	Glu	Gly	Ala	Ser	Ser	Ser	Gly	Gly	Ser
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Ser	Pro	Leu	Ser	Pro	Arg	Ser	Leu	Ser	Ser	Asn	Pro	Ser	Ser	Arg	Asp
				485					490					495	
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10/155

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Arg	Ala	Gly	Asp	Leu	Ile	Thr	His	Ile	Asn	Gly	Glu	Ser	Val	Leu	Gly
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Leu	Val	His	Met	Asp	Val	Val	Glu	Leu	Leu	Leu	Lys	Ser	Gly	Asn	Lys
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Pro	Ala	Arg	Lys	Asn	Val	Ala	Lys	Gly	Arg	Met	Ala	Arg	Arg	Ser	Lys
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Lys	Ile	Ser	Lys	Gln	Thr	Ser	Val	Leu	His	Thr	Ser	Arg	Ser	Phe	Ser
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Ser	Gly	Leu	His	His	Ser	Leu	Ser	Ser	Ser	Glu	Ser	Leu	Pro	Gly	Ser
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Pro	Thr	His	Ser	Leu	Ser	Pro	Ser	Pro	Thr	Thr	Pro	Cys	Arg	Ser	Pro
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Pro	Ser	Ser	Leu	His	Gly	Leu	Ala	Ala	Lys	Leu	Gly	Pro	Pro	Arg	Pro
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Lys	Thr	Gly	Arg	Arg	Lys	Ser	Thr	Ser	Ser	Ile	Pro	Pro	Ser	Pro	Leu
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Ala	Cys	Pro	Pro	Ile	Ser	Ala	Pro	Pro	Pro	Arg	Ser	Pro	Ser	Pro	Leu
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Pro	Gly	His	Pro	Pro	Ala	Pro	Ala	Arg	Ser	Pro	Arg	Leu	Arg	Arg	Gly
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Gln	Glu	Val	Ser	Phe	Asp	Glu	Pro	Gln	Glu	Glu	Ala	Thr	Gly	Leu	Pro
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Thr	Ser	Val	Pro	Gln	Ile	Ala	Val	Glu	Gly	Glu	Glu	Ala	Thr	Glu	Ala
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Gln	Asn	Arg	Gln	Leu	Pro	Ser	Thr	Thr	Arg	Gly	Leu	Met	Ala	Ser	Leu
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Pro	His	Cys	Asp	Val	Ile	Val	Pro	Ser	Ala	Leu	Pro	Asn	Pro	Gly	Ala
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Ser	Leu	Ser	Leu	Ser	Cys	Leu	Gln	Leu	Tyr	Ala	Pro	Gly	Leu	Ser	Pro
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Asp	Thr	Ile	Met	Glu	Cys	Ala	Met	Gly	Asp	Arg	Gly	Met	Gln	Leu	Met
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His	Ala	Asn	Ala	Gln	Arg	Thr	Asp	Ala	Leu	Gln	Pro	Pro	His	Glu	Glu
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Ser	Pro	Ala	Ser	Ala	Ser	Arg	Val	Ala	Gly	Thr	Thr	Ser	Gly	Cys	Tyr
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His	Thr	Trp	Leu	Phe	Phe	Phe	Phe	Tyr	Glu	Pro	Arg	Ser	Arg	His	Cys
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Thr	Pro	Ala	Trp	Ala	Thr	Val	Arg	Asp	Ser	Val	Ser	Asn	Lys	Gln	Lys
		995					1000					1005			
Asp	Pro	Thr	Leu	Leu	Cys	Ser	Phe	Gly	Pro	Ser	Met	Thr	Gly	Ser	Glu
	1010					1015					1020				
Leu	Gly	Leu	Ile	Thr	Ser	Asn	Trp	Thr	Trp	Ser	Arg	Arg	Val	Cys	Ser
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11/155

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 Pro Pro Ser Leu Leu Trp Val Lys Lys Lys Trp Ser Leu Gly Pro Arg
 20 25 30

aag cag aag gaa gga aga gac cct ttt att ttt ttg gtt agt gaa tgt 144
 Lys Gln Lys Glu Gly Arg Asp Pro Phe Ile Phe Leu Val Ser Glu Cys
 35 40 45

cag cca cca atg aca cgt gct aat act atg aca tca gag ccc acc atg 192
 Gln Pro Pro Met Thr Arg Ala Asn Thr Met Thr Ser Glu Pro Thr Met
 50 55 60

tta gcc att tgc cga aca agc aac cgg aaa agc tta ata ggc aat ggg 240
 Leu Ala Ile Cys Arg Thr Ser Asn Arg Lys Ser Leu Ile Gly Asn Gly
 65 70 75 80

cag tca cca gca ttg cct cga cca cac tca cct ctc tct gct cat gca 288
 Gln Ser Pro Ala Leu Pro Arg Pro His Ser Pro Leu Ser Ala His Ala
 85 90 95

ggt aat tgc cct caa gat agt cca aga aat ttc tcc ccc agt gcc tca 336
 Gly Asn Cys Pro Gln Asp Ser Pro Arg Asn Phe Ser Pro Ser Ala Ser
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gcc cat ttt tca ttt gca cgg agg act gat gga cgc cgc tgg tcg ttg 384
 Ala His Phe Ser Phe Ala Arg Arg Thr Asp Gly Arg Arg Trp Ser Leu
 115 120 125

gct tct ctc cct tcc tct ggc tat ggg aca aac aca ccc agc tct acg 432
 Ala Ser Leu Pro Ser Ser Gly Tyr Gly Thr Asn Thr Pro Ser Ser Thr
 130 135 140

gtc tct tca tcc tgt tcc tcc cag gag aag ttg cat cag tta cca tac 480
 Val Ser Ser Ser Cys Ser Ser Gln Glu Lys Leu His Gln Leu Pro Tyr
 145 150 155 160

caa cca aca cca gac gag tta cac ttc tta tca aaa cat ttc tgt acc 528
 Gln Pro Thr Pro Asp Glu Leu His Phe Leu Ser Lys His Phe Cys Thr
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 Thr Glu Ser Ile Ala Thr Glu Asn Arg Cys Arg Asn Thr Pro Met Arg
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12/155

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cat	gaa	ata	att	atg	atg	aac	cat	gtc	tac	aaa	gaa	agg	ttc	cca	aag	672
His	Glu	Ile	Ile	Met	Met	Asn	His	Val	Tyr	Lys	Glu	Arg	Phe	Pro	Lys	
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Ser	Pro	Asp	Asn	Val	Leu	Pro	Leu	Ala	Asp	Gly	Val	Leu	Ser	Phe	Thr	
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cac	cac	cag	att	att	gaa	ctg	gct	cga	gat	tgc	ttg	gat	aaa	tcc	cac	816
His	His	Gln	Ile	Ile	Glu	Leu	Ala	Arg	Asp	Cys	Leu	Asp	Lys	Ser	His	
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cag	ggc	ctc	atc	acc	tca	cga	tac	ttc	ctt	gaa	tta	cag	cac	aaa	tta	864
Gln	Gly	Leu	Ile	Thr	Ser	Arg	Tyr	Phe	Leu	Glu	Leu	Gln	His	Lys	Leu	
	275						280					285				
gat	aag	ttg	cta	cag	gag	gct	cat	gat	cgt	tca	gaa	agt	gga	gaa	ttg	912
Asp	Lys	Leu	Leu	Gln	Glu	Ala	His	Asp	Arg	Ser	Glu	Ser	Gly	Glu	Leu	
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gca	ttt	att	aaa	caa	cta	gtt	cga	aag	atc	cta	att	gtt	att	gcc	cgc	960
Ala	Phe	Ile	Lys	Gln	Leu	Val	Arg	Lys	Ile	Leu	Ile	Val	Ile	Ala	Arg	
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cct	gct	cgg	tta	tta	gag	tgc	ctg	gaa	ttt	gat	ccg	gaa	gaa	ttt	tac	1008
Pro	Ala	Arg	Leu	Leu	Glu	Cys	Leu	Glu	Phe	Asp	Pro	Glu	Glu	Phe	Tyr	
			325						330					335		
tac	cta	ttg	gaa	gca	gca	gaa	ggc	cat	gcc	aaa	gaa	gga	cag	ggg	att	1056
Tyr	Leu	Leu	Glu	Ala	Ala	Glu	Gly	His	Ala	Lys	Glu	Gly	Gln	Gly	Ile	
		340					345						350			
aaa	acc	gac	att	ccc	agg	tac	atc	att	agc	caa	ctg	gga	ctc	aat	aag	1104
Lys	Thr	Asp	Ile	Pro	Arg	Tyr	Ile	Ile	Ser	Gln	Leu	Gly	Leu	Asn	Lys	
		355					360					365				
gat	ccc	ttg	gaa	gaa	atg	gct	cat	ttg	gga	aac	tac	gat	agt	ggg	aca	1152
Asp	Pro	Leu	Glu	Glu	Met	Ala	His	Leu	Gly	Asn	Tyr	Asp	Ser	Gly	Thr	
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gca	gaa	aca	cca	gaa	aca	gat	gaa	tca	gtg	agt	agc	tct	aat	gcc	tcc	1200
Ala	Glu	Thr	Pro	Glu	Thr	Asp	Glu	Ser	Val	Ser	Ser	Ser	Asn	Ala	Ser	
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ctg	aaa	ctt	cga	agg	aaa	cct	cgg	gaa	agt	gat	ttt	gaa	acg	att	aaa	1248
Leu	Lys	Leu	Arg	Arg	Lys	Pro	Arg	Glu	Ser	Asp	Phe	Glu	Thr	Ile	Lys	
			405						410					415		
ttg	att	agc	aat	gga	gcc	tat	ggg	gca	gtc	tac	ttt	gtt	cgg	cat	aaa	1296
Leu	Ile	Ser	Asn	Gly	Ala	Tyr	Gly	Ala	Val	Tyr	Phe	Val	Arg	His	Lys	
			420					425					430			

13/155

gaa tcc cgg cag agg ttt gcc atg aag aag att aat aaa cag aac ctc	1344
Glu Ser Arg Gln Arg Phe Ala Met Lys Lys Ile Asn Lys Gln Asn Leu	
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atc ctt cga aac cag atc cag cag gcc ttt gtg gag cgg gat atc ctg	1392
Ile Leu Arg Asn Gln Ile Gln Gln Ala Phe Val Glu Arg Asp Ile Leu	
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act ttt gca gaa aac ccc ttt gtt gtc agc atg tat tgc tcc ttt gaa	1440
Thr Phe Ala Glu Asn Pro Phe Val Val Ser Met Tyr Cys Ser Phe Glu	
465 470 475 480	
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Thr Arg Arg His Leu Cys Met Val Met Glu Tyr Val Glu Gly Gly Asp	
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Cys Ala Thr Leu Met Lys Asn Met Gly Pro Leu Pro Val Asp Met Ala	
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Arg Met Tyr Phe Ala Glu Thr Val Leu Ala Leu Glu Tyr Leu His Asn	
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tat gga att gta cac agg gat ttg aaa cca gac aac ttg ttg gtt acc	1632
Tyr Gly Ile Val His Arg Asp Leu Lys Pro Asp Asn Leu Leu Val Thr	
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Ser Met Gly His Ile Lys Leu Thr Asp Phe Gly Leu Ser Lys Val Gly	
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cta atg agc atg act acc aac ctt tac gag ggt cat att gag aag gat	1728
Leu Met Ser Met Thr Thr Asn Leu Tyr Glu Gly His Ile Glu Lys Asp	
565 570 575	
gct aga gag ttc ctg gat aaa cag gtc tgt ggc aca cct gaa tac att	1776
Ala Arg Glu Phe Leu Asp Lys Gln Val Cys Gly Thr Pro Glu Tyr Ile	
580 585 590	
gca cca gaa gtg att ctg agg cag ggt tat gga aag ccg gtg gac tgg	1824
Ala Pro Glu Val Ile Leu Arg Gln Gly Tyr Gly Lys Pro Val Asp Trp	
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tgg gcc atg ggg att atc ctc tat gaa ttt ctg gtt gga tgc gtg cca	1872
Trp Ala Met Gly Ile Ile Leu Tyr Glu Phe Leu Val Gly Cys Val Pro	
610 615 620	
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Phe Phe Gly Asp Thr Pro Glu Glu Leu Phe Gly Gln Val Ile Ser Asp	
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gag atc aac tgg cct gag aag gat gag gca ccc cca cct gat gcc cag	1968
Glu Ile Asn Trp Pro Glu Lys Asp Glu Ala Pro Pro Pro Asp Ala Gln	
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Asp Leu Ile Thr Leu Leu Leu Arg Gln Asn Pro Leu Glu Arg Leu Gly	
660 665 670	

14/155

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gac tgg aac agt ttg ctg aga cag aag gca gaa ttt att ccc caa ctg	2112
Asp Trp Asn Ser Leu Leu Arg Gln Lys Ala Glu Phe Ile Pro Gln Leu	
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Gln Pro Pro Met Thr Arg Ala Asn Thr Met Thr Ser Glu Pro Thr Met	
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Gln Ser Pro Ala Leu Pro Arg Pro His Ser Pro Leu Ser Ala His Ala	
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Gly Asn Cys Pro Gln Asp Ser Pro Arg Asn Phe Ser Pro Ser Ala Ser	
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Ala His Phe Ser Phe Ala Arg Arg Thr Asp Gly Arg Arg Trp Ser Leu	
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Ala Ser Leu Pro Ser Ser Gly Tyr Gly Thr Asn Thr Pro Ser Ser Thr	
130 135 140	
Val Ser Ser Ser Cys Ser Ser Gln Glu Lys Leu His Gln Leu Pro Tyr	
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Gln Pro Thr Pro Asp Glu Leu His Phe Leu Ser Lys His Phe Cys Thr	
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Thr Glu Ser Ile Ala Thr Glu Asn Arg Cys Arg Asn Thr Pro Met Arg	
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Pro Arg Ser Arg Ser Leu Ser Pro Gly Arg Ser Pro Ala Cys Cys Asp	
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His Glu Ile Ile Met Met Asn His Val Tyr Lys Glu Arg Phe Pro Lys	
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Ala Thr Ala Gln Met Glu Glu Arg Leu Lys Glu Ile Ile Thr Ser Tyr	
225 230 235 240	
Ser Pro Asp Asn Val Leu Pro Leu Ala Asp Gly Val Leu Ser Phe Thr	
245 250 255	
His His Gln Ile Ile Glu Leu Ala Arg Asp Cys Leu Asp Lys Ser His	
260 265 270	
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275 280 285	
Asp Lys Leu Leu Gln Glu Ala His Asp Arg Ser Glu Ser Gly Glu Leu	
290 295 300	
Ala Phe Ile Lys Gln Leu Val Arg Lys Ile Leu Ile Val Ile Ala Arg	
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Pro Ala Arg Leu Leu Glu Cys Leu Glu Phe Asp Pro Glu Glu Phe Tyr	
325 330 335	

15/155

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Lys Thr Asp Ile Pro Arg Tyr Ile Ile Ser Gln Leu Gly Leu Asn Lys
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Asp Pro Leu Glu Glu Met Ala His Leu Gly Asn Tyr Asp Ser Gly Thr
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Ala Glu Thr Pro Glu Thr Asp Glu Ser Val Ser Ser Ser Asn Ala Ser
385      390      395      400
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Leu Ile Ser Asn Gly Ala Tyr Gly Ala Val Tyr Phe Val Arg His Lys
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Glu Ser Arg Gln Arg Phe Ala Met Lys Lys Ile Asn Lys Gln Asn Leu
      435      440      445
Ile Leu Arg Asn Gln Ile Gln Gln Ala Phe Val Glu Arg Asp Ile Leu
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Thr Phe Ala Glu Asn Pro Phe Val Val Ser Met Tyr Cys Ser Phe Glu
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Thr Arg Arg His Leu Cys Met Val Met Glu Tyr Val Glu Gly Gly Asp
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Cys Ala Thr Leu Met Lys Asn Met Gly Pro Leu Pro Val Asp Met Ala
      500      505      510
Arg Met Tyr Phe Ala Glu Thr Val Leu Ala Leu Glu Tyr Leu His Asn
      515      520      525
Tyr Gly Ile Val His Arg Asp Leu Lys Pro Asp Asn Leu Leu Val Thr
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Ser Met Gly His Ile Lys Leu Thr Asp Phe Gly Leu Ser Lys Val Gly
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Leu Met Ser Met Thr Thr Asn Leu Tyr Glu Gly His Ile Glu Lys Asp
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Ala Arg Glu Phe Leu Asp Lys Gln Val Cys Gly Thr Pro Glu Tyr Ile
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Thr Gly Gly Ala Tyr Glu Val Lys Gln His Arg Phe Phe Arg Ser Leu
      675      680      685
Asp Trp Asn Ser Leu Leu Arg Gln Lys Ala Glu Phe Ile Pro Gln Leu
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16/155

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Gly Gly Cys Pro Gly Leu Asp Gly Leu Leu Asp Leu Leu Leu Ala Leu	
20 25 30	
cac cac gag ctc agc agc ggc ccc cta cgg cgg gag cgc agc gtg gcg	144
His His Glu Leu Ser Ser Gly Pro Leu Arg Arg Glu Arg Ser Val Ala	
35 40 45	
cag ttc ctg agc tgg gcc agc ccc ttc gta tca aag gtg aaa gaa ctg	192
Gln Phe Leu Ser Trp Ala Ser Pro Phe Val Ser Lys Val Lys Glu Leu	
50 55 60	
cgt ctg cag aga gat gac ttt gag atc ttg aag gtg atc ggc cga gga	240
Arg Leu Gln Arg Asp Asp Phe Glu Ile Leu Lys Val Ile Gly Arg Gly	
65 70 75 80	
gcc ttt ggg gag gtc acc gtg gtg agg cag agg gac act ggg cag att	288
Ala Phe Gly Glu Val Thr Val Val Arg Gln Arg Asp Thr Gly Gln Ile	
85 90 95	
ttt gcc atg aaa atg ctg cac aag tgg gag atg ctg aag agg gct gag	336
Phe Ala Met Lys Met Leu His Lys Trp Glu Met Leu Lys Arg Ala Glu	
100 105 110	
gtc acc tgt ttc cgg gag gag cgg gat gtg ctc gtg aaa ggg gac agc	384
Val Thr Cys Phe Arg Glu Glu Arg Asp Val Leu Val Lys Gly Asp Ser	
115 120 125	
cgt tgg gtg acc act ctg cac tat gcc ttc caa gac gag gag tac ctg	432
Arg Trp Val Thr Thr Leu His Tyr Ala Phe Gln Asp Glu Glu Tyr Leu	
130 135 140	
tac ctt gtg atg gac tac tat gct ggt ggg gac ctc ctg acg ctg ctg	480
Tyr Leu Val Met Asp Tyr Tyr Ala Gly Gly Asp Leu Leu Thr Leu Leu	
145 150 155 160	
agc cgc ttc gag gac cgt ctc ccg ccc gag ctg gcc cag ttc tac ctg	528
Ser Arg Phe Glu Asp Arg Leu Pro Pro Glu Leu Ala Gln Phe Tyr Leu	
165 170 175	
gct gag atg gtg ctg gcc atc cac tcg ctg cac cag ctg ggt tat gtc	576
Ala Glu Met Val Leu Ala Ile His Ser Leu His Gln Leu Gly Tyr Val	
180 185 190	
cac agg gat gtc aag cca gac aac gtc ctg ctg gat gtg aac ggg cac	624
His Arg Asp Val Lys Pro Asp Asn Val Leu Leu Asp Val Asn Gly His	
195 200 205	
att cgc ctg gct gac ttc ggc tcc tgc ctg cgt ctc aac acc aac ggc	672
Ile Arg Leu Ala Asp Phe Gly Ser Cys Leu Arg Leu Asn Thr Asn Gly	
210 215 220	
atg gtg gat tca tca gtg gca gta ggg acg ccg gac tat atc tcc cct	720
Met Val Asp Ser Ser Val Ala Val Gly Thr Pro Asp Tyr Ile Ser Pro	
225 230 235 240	

17/155

gag atc ctg cag gcc atg gag gag ggc aag ggc cac tac ggc cca cag	768
Glu Ile Leu Gln Ala Met Glu Glu Gly Lys Gly His Tyr Gly Pro Gln	
245 250 255	
tgt gac tgg tgg tcg ctt gga gtc tgc gcc tat gag ctg ctc ttt ggg	816
Cys Asp Trp Trp Ser Leu Gly Val Cys Ala Tyr Glu Leu Leu Phe Gly	
260 265 270	
gag acg ccc ttc tat gct gag tcc ttg gtg gaa acc tac ggc aag atc	864
Glu Thr Pro Phe Tyr Ala Glu Ser Leu Val Glu Thr Tyr Gly Lys Ile	
275 280 285	
atg aac cac gag gac cac ctg cag ttc ccc ccg gac gtg cct gac gtg	912
Met Asn His Glu Asp His Leu Gln Phe Pro Pro Asp Val Pro Asp Val	
290 295 300	
cca gcc agc gcc caa gac ctg atc cgc cag ctg ctg tgt cgc cag gaa	960
Pro Ala Ser Ala Gln Asp Leu Ile Arg Gln Leu Leu Cys Arg Gln Glu	
305 310 315 320	
gag cgg cta ggc cgt ggt ggg ctg gat gac ttc cgg aac cat cct ttc	1008
Glu Arg Leu Gly Arg Gly Gly Leu Asp Asp Phe Arg Asn His Pro Phe	
325 330 335	
ttc gaa ggc gtg gac tgg gag cgg ctg gcg agc agc acg gcc ccc tat	1056
Phe Glu Gly Val Asp Trp Glu Arg Leu Ala Ser Ser Thr Ala Pro Tyr	
340 345 350	
att cct gag ctg cgg gga ccc atg gac acc tcc aac ttt gat gtg gat	1104
Ile Pro Glu Leu Arg Gly Pro Met Asp Thr Ser Asn Phe Asp Val Asp	
355 360 365	
gac gac acc ctc aac cat cca gtg agt ggc aaa ggc cac tgc agg agg	1152
Asp Asp Thr Leu Asn His Pro Val Ser Gly Lys Gly His Cys Arg Arg	
370 375 380	
gga gct gcc cta ccc cct tgt ttc tac caa caa aca tgg ccc ctg tcc	1200
Gly Ala Ala Leu Pro Pro Cys Phe Tyr Gln Gln Thr Trp Pro Leu Ser	
385 390 395 400	
ccc tac agt cac agt cct gag agc agc tct gag gct tgg gct gcc ctg	1248
Pro Tyr Ser His Ser Pro Glu Ser Ser Ser Glu Ala Trp Ala Ala Leu	
405 410 415	
gag cgg aag ctc cag tgt ctg gag cag gag aag gtg gag ctg agc agg	1296
Glu Arg Lys Leu Gln Cys Leu Glu Gln Glu Lys Val Glu Leu Ser Arg	
420 425 430	
aag cac caa ggt act ggg agc ggc tgg gcc ggg cct ggg tgt gct ggc	1344
Lys His Gln Gly Thr Gly Ser Gly Trp Ala Gly Pro Gly Cys Ala Gly	
435 440 445	
cct agg ggc tgc tgc tgc ggg aat gga gga gtg gac tca cct gtg ggt	1392
Pro Arg Gly Cys Cys Cys Gly Asn Gly Gly Val Asp Ser Pro Val Gly	
450 455 460	
acc acc tcc cct cca gag gcc ctg cac gcc ccc aca gac cat cgg gag	1440
Thr Thr Ser Pro Pro Glu Ala Leu His Ala Pro Thr Asp His Arg Glu	
465 470 475 480	

18/155

ctg	gag	cag	cta	cgg	aag	gaa	gtg	cag	act	ctg	cgg	gac	agg	ctg	cca	1488
Leu	Glu	Gln	Leu	Arg	Lys	Glu	Val	Gln	Thr	Leu	Arg	Asp	Arg	Leu	Pro	
				485					490					495		
ggt	atc	cct	tcc	gcc	cac	ccc	ccc	ccc	ccc	ccc	ccc	ggg	gct	gag	tcc	1536
Gly	Ile	Pro	Ser	Ala	His	Pro	Pro	Pro	Pro	Pro	Pro	Gly	Ala	Glu	Ser	
			500					505					510			
cac	ctg	ggc	tcg	ggt	cct	gcc	ctg	ccc	tgg	aca	agc	tgt	atg	atc	ctg	1584
His	Leu	Gly	Ser	Gly	Pro	Ala	Leu	Pro	Trp	Thr	Ser	Cys	Met	Ile	Leu	
		515					520					525				
gga	gag	cat	ttt	ata	ctc	tct	gag	ccc	gcg	tgt	ggg	aaa	cag	gcc	aag	1632
Gly	Glu	His	Phe	Ile	Leu	Ser	Glu	Pro	Ala	Cys	Gly	Lys	Gln	Ala	Lys	
	530					535					540					
gag	act	tgc	tcc	tgg	gct	gag	agg	ctg	ggg	ccg	cca	gca	ctc	gag	ggg	1680
Glu	Thr	Cys	Ser	Trp	Ala	Glu	Arg	Leu	Gly	Pro	Pro	Ala	Leu	Glu	Gly	
545					550				555						560	
cag	cag	gag	gag	ctg	ctt	cag	agg	cta	cag	gag	gcc	cag	gag	aga	gag	1728
Gln	Gln	Glu	Glu	Leu	Leu	Gln	Arg	Leu	Gln	Glu	Ala	Gln	Glu	Arg	Glu	
				565					570					575		
gcg	gcc	aca	gct	agc	cag	acc	cgg	gcc	ctg	agc	tcc	cag	ctg	gag	gaa	1776
Ala	Ala	Thr	Ala	Ser	Gln	Thr	Arg	Ala	Leu	Ser	Ser	Gln	Leu	Glu	Glu	
			580					585					590			
gcc	cgg	gct	gcc	cag	agg	gag	gcg	cgg	cga	ctg	cag	aag	atg	gag	gcc	1824
Ala	Arg	Ala	Ala	Gln	Arg	Glu	Ala	Arg	Arg	Leu	Gln	Lys	Met	Glu	Ala	
		595				600						605				
tcg	gcc	agg	ctg	gag	ctg	cag	tca	gcg	ctg	gag	gcc	gag	atc	cgc	gcc	1872
Ser	Ala	Arg	Leu	Glu	Leu	Gln	Ser	Ala	Leu	Glu	Ala	Glu	Ile	Arg	Ala	
	610					615					620					
aag	cag	ggc	ctg	cag	gag	cgg	ctg	aca	cag	gtg	cag	gag	gcc	cag	ctg	1920
Lys	Gln	Gly	Leu	Gln	Glu	Arg	Leu	Thr	Gln	Val	Gln	Glu	Ala	Gln	Leu	
625					630					635					640	
cag	gct	gag	cgg	gtg	agt	gcc	tgg	gat	gag	atg	gag	cag	cca	cca	tcc	1968
Gln	Ala	Glu	Arg	Val	Ser	Ala	Trp	Asp	Glu	Met	Glu	Gln	Pro	Pro	Ser	
				645					650					655		
acc	tcc	cca	tgc	tgt	ccc	agc	tct	ggc	cac	tgt	ccc	ccc	act	tca	tac	2016
Thr	Ser	Pro	Cys	Cys	Pro	Ser	Ser	Gly	His	Cys	Pro	Pro	Thr	Ser	Tyr	
			660					665					670			
tgc	cct	ctt	ggg	cca	gcc	cac	aac	cac	agc	acg	ctt	tcc	aca	gcg	agg	2064
Cys	Pro	Leu	Gly	Pro	Ala	His	Asn	His	Ser	Thr	Leu	Ser	Thr	Ala	Arg	
		675					680					685				
ggg	agc	ggg	aac	gct	ggc	tgc	agg	tgc	tgg	gtg	agc	tgc	agc	ggc	tgc	2112
Gly	Ser	Gly	Asn	Ala	Gly	Cys	Arg	Cys	Trp	Val	Ser	Cys	Ser	Gly	Cys	
	690					695					700					
tgc	tgg	acg	cgc	ggc	caa	gac	ccc	ggc	ccg	tgt	aca	cac	tca	agg	agg	2160
Cys	Trp	Thr	Arg	Gly	Gln	Asp	Pro	Gly	Pro	Cys	Thr	His	Ser	Arg	Arg	
705					710					715					720	

19/155

ctt acg aca acg ggc tgc cgc tgc tgc ctc aca cgc tct gcg ctg cca 2208
 Leu Thr Thr Thr Gly Cys Arg Cys Cys Leu Thr Arg Ser Ala Leu Pro
 725 730 735
 tcc tcg gtg agc tgg tgg agg gga ctg gag gaa gca gtc cag gcc tgc 2256
 Ser Ser Val Ser Trp Trp Arg Gly Leu Glu Glu Ala Val Gln Ala Cys
 740 745 750
 ggg agt gct ggg ctg gaa gag agg ggc aga gtg tcc ttc agc cag acc 2304
 Gly Ser Ala Gly Leu Glu Glu Arg Gly Arg Val Ser Phe Ser Gln Thr
 755 760 765
 aac gtt act cag ggc tcc tcc cag ctt tct ccc tct tac ccc gtc ccc 2352
 Asn Val Thr Gln Gly Ser Ser Gln Leu Ser Pro Ser Tyr Pro Val Pro
 770 775 780
 agc cac cct ggt ctc act cat tgc agc ctt gat ctc ctg ggc tca agt 2400
 Ser His Pro Gly Leu Thr His Cys Ser Leu Asp Leu Leu Gly Ser Ser
 785 790 795 800
 aat cct cct gct tca gcc tct tgt gaa aag caa aga cga agc gaa cca 2448
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 tct ctc tcc att gtg
 Ser Leu Ser Ile Val 2463
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<211> 821

<212> PRT

<213> Homo sapiens

<400> 8

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 20 25 30
 His His Glu Leu Ser Ser Gly Pro Leu Arg Arg Glu Arg Ser Val Ala
 35 40 45
 Gln Phe Leu Ser Trp Ala Ser Pro Phe Val Ser Lys Val Lys Glu Leu
 50 55 60
 Arg Leu Gln Arg Asp Asp Phe Glu Ile Leu Lys Val Ile Gly Arg Gly
 65 70 75 80
 Ala Phe Gly Glu Val Thr Val Val Arg Gln Arg Asp Thr Gly Gln Ile
 85 90 95
 Phe Ala Met Lys Met Leu His Lys Trp Glu Met Leu Lys Arg Ala Glu
 100 105 110
 Val Thr Cys Phe Arg Glu Glu Arg Asp Val Leu Val Lys Gly Asp Ser
 115 120 125
 Arg Trp Val Thr Thr Leu His Tyr Ala Phe Gln Asp Glu Glu Tyr Leu
 130 135 140
 Tyr Leu Val Met Asp Tyr Tyr Ala Gly Gly Asp Leu Leu Thr Leu Leu
 145 150 155 160
 Ser Arg Phe Glu Asp Arg Leu Pro Pro Glu Leu Ala Gln Phe Tyr Leu
 165 170 175
 Ala Glu Met Val Leu Ala Ile His Ser Leu His Gln Leu Gly Tyr Val
 180 185 190
 His Arg Asp Val Lys Pro Asp Asn Val Leu Leu Asp Val Asn Gly His
 195 200 205

20/155

Ile	Arg	Leu	Ala	Asp	Phe	Gly	Ser	Cys	Leu	Arg	Leu	Asn	Thr	Asn	Gly
	210					215					220				
Met	Val	Asp	Ser	Ser	Val	Ala	Val	Gly	Thr	Pro	Asp	Tyr	Ile	Ser	Pro
225					230					235					240
Glu	Ile	Leu	Gln	Ala	Met	Glu	Glu	Gly	Lys	Gly	His	Tyr	Gly	Pro	Gln
				245					250					255	
Cys	Asp	Trp	Trp	Ser	Leu	Gly	Val	Cys	Ala	Tyr	Glu	Leu	Leu	Phe	Gly
			260					265					270		
Glu	Thr	Pro	Phe	Tyr	Ala	Glu	Ser	Leu	Val	Glu	Thr	Tyr	Gly	Lys	Ile
		275					280					285			
Met	Asn	His	Glu	Asp	His	Leu	Gln	Phe	Pro	Pro	Asp	Val	Pro	Asp	Val
	290					295					300				
Pro	Ala	Ser	Ala	Gln	Asp	Leu	Ile	Arg	Gln	Leu	Leu	Cys	Arg	Gln	Glu
305					310					315					320
Glu	Arg	Leu	Gly	Arg	Gly	Gly	Leu	Asp	Asp	Phe	Arg	Asn	His	Pro	Phe
				325					330					335	
Phe	Glu	Gly	Val	Asp	Trp	Glu	Arg	Leu	Ala	Ser	Ser	Thr	Ala	Pro	Tyr
			340					345					350		
Ile	Pro	Glu	Leu	Arg	Gly	Pro	Met	Asp	Thr	Ser	Asn	Phe	Asp	Val	Asp
		355					360					365			
Asp	Asp	Thr	Leu	Asn	His	Pro	Val	Ser	Gly	Lys	Gly	His	Cys	Arg	Arg
	370					375					380				
Gly	Ala	Ala	Leu	Pro	Pro	Cys	Phe	Tyr	Gln	Gln	Thr	Trp	Pro	Leu	Ser
385					390					395					400
Pro	Tyr	Ser	His	Ser	Pro	Glu	Ser	Ser	Ser	Glu	Ala	Trp	Ala	Ala	Leu
				405					410					415	
Glu	Arg	Lys	Leu	Gln	Cys	Leu	Glu	Gln	Glu	Lys	Val	Glu	Leu	Ser	Arg
			420					425				430			
Lys	His	Gln	Gly	Thr	Gly	Ser	Gly	Trp	Ala	Gly	Pro	Gly	Cys	Ala	Gly
		435					440					445			
Pro	Arg	Gly	Cys	Cys	Cys	Gly	Asn	Gly	Gly	Val	Asp	Ser	Pro	Val	Gly
	450					455					460				
Thr	Thr	Ser	Pro	Pro	Glu	Ala	Leu	His	Ala	Pro	Thr	Asp	His	Arg	Glu
465					470					475					480
Leu	Glu	Gln	Leu	Arg	Lys	Glu	Val	Gln	Thr	Leu	Arg	Asp	Arg	Leu	Pro
				485					490					495	
Gly	Ile	Pro	Ser	Ala	His	Pro	Pro	Pro	Pro	Pro	Pro	Gly	Ala	Glu	Ser
			500					505					510		
His	Leu	Gly	Ser	Gly	Pro	Ala	Leu	Pro	Trp	Thr	Ser	Cys	Met	Ile	Leu
		515					520					525			
Gly	Glu	His	Phe	Ile	Leu	Ser	Glu	Pro	Ala	Cys	Gly	Lys	Gln	Ala	Lys
	530					535					540				
Glu	Thr	Cys	Ser	Trp	Ala	Glu	Arg	Leu	Gly	Pro	Pro	Ala	Leu	Glu	Gly
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Gln	Gln	Glu	Glu	Leu	Leu	Gln	Arg	Leu	Gln	Glu	Ala	Gln	Glu	Arg	Glu
				565					570					575	
Ala	Ala	Thr	Ala	Ser	Gln	Thr	Arg	Ala	Leu	Ser	Ser	Gln	Leu	Glu	Glu
			580					585					590		
Ala	Arg	Ala	Ala	Gln	Arg	Glu	Ala	Arg	Arg	Leu	Gln	Lys	Met	Glu	Ala
		595					600					605			
Ser	Ala	Arg	Leu	Glu	Leu	Gln	Ser	Ala	Leu	Glu	Ala	Glu	Ile	Arg	Ala
	610					615					620				
Lys	Gln	Gly	Leu	Gln	Glu	Arg	Leu	Thr	Gln	Val	Gln	Glu	Ala	Gln	Leu
625					630					635					640
Gln	Ala	Glu	Arg	Val	Ser	Ala	Trp	Asp	Glu	Met	Glu	Gln	Pro	Pro	Ser
				645					650					655	
Thr	Ser	Pro	Cys	Cys	Pro	Ser	Ser	Gly	His	Cys	Pro	Pro	Thr	Ser	Tyr
		660						665					670		
Cys	Pro	Leu	Gly	Pro	Ala	His	Asn	His	Ser	Thr	Leu	Ser	Thr	Ala	Arg
		675					680					685			
Gly	Ser	Gly	Asn	Ala	Gly	Cys	Arg	Cys	Trp	Val	Ser	Cys	Ser	Gly	Cys
	690					695					700				

21/155

Cys Trp Thr Arg Gly Gln Asp Pro Gly Pro Cys Thr His Ser Arg Arg
 705 710 715 720
 Leu Thr Thr Thr Gly Cys Arg Cys Cys Leu Thr Arg Ser Ala Leu Pro
 725 730 735
 Ser Ser Val Ser Trp Trp Arg Gly Leu Glu Glu Ala Val Gln Ala Cys
 740 745 750
 Gly Ser Ala Gly Leu Glu Glu Arg Gly Arg Val Ser Phe Ser Gln Thr
 755 760 765
 Asn Val Thr Gln Gly Ser Ser Gln Leu Ser Pro Ser Tyr Pro Val Pro
 770 775 780
 Ser His Pro Gly Leu Thr His Cys Ser Leu Asp Leu Leu Gly Ser Ser
 785 790 795 800
 Asn Pro Pro Ala Ser Ala Ser Cys Glu Lys Gln Arg Arg Ser Glu Pro
 805 810 815
 Ser Leu Ser Ile Val
 820

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 Thr Val Phe Lys Gly Arg Ser Lys Leu Thr Glu Asn Leu Val Ala Leu
 20 25 30

 aaa gag atc cgg ctg gag cac gag gag gga ggc ccc tgc act gcc atc 144
 Lys Glu Ile Arg Leu Glu His Glu Glu Gly Ala Pro Cys Thr Ala Ile
 35 40 45

 cga gag gtg tct ctg ctg aag aac ctg aag cac gcc aat att gtg acc 192
 Arg Glu Val Ser Leu Leu Lys Asn Leu Lys His Ala Asn Ile Val Thr
 50 55 60

 ctg cat gac ctc atc cac aca gat cgg tcc ctc acc ctg gtg ttt gag 240
 Leu His Asp Leu Ile His Thr Asp Arg Ser Leu Thr Leu Val Phe Glu
 65 70 75 80

 tac ctg gtg aga gac agt gac ctg aag cag tat ctg gac cac tgt ggg 288
 Tyr Leu Val Arg Asp Ser Asp Leu Lys Gln Tyr Leu Asp His Cys Gly
 85 90 95

 aac ctc atg agc atg cac aac gtc aag att ttc atg ttc cag ctg ctc 336
 Asn Leu Met Ser Met His Asn Val Lys Ile Phe Met Phe Gln Leu Leu
 100 105 110

 cgg ggc ctc gcc tac tgt cac cac cgc aag atc ctg cac cgg gag ctg 384
 Arg Gly Leu Ala Tyr Cys His His Arg Lys Ile Leu His Arg Glu Leu
 115 120 125

22/155

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aag ccc cag aac ctg ctc atc aac gag agg ggg gag ctg aag ctg gcc 432
Lys Pro Gln Asn Leu Leu Ile Asn Glu Arg Gly Glu Leu Lys Leu Ala
130 135 140

gac ttt gga ctg gcc agg gcc aag tca gtg ccc aca aag act tac tcc 480
Asp Phe Gly Leu Ala Arg Ala Lys Ser Val Pro Thr Lys Thr Tyr Ser
145 150 155 160

aat gag gtg gtg acc ctg tgg tac agg ccc ccc gat gtg ctg ctg gga 528
Asn Glu Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Val Leu Leu Gly
165 170 175

tcc aca gag tac tcc acc ccc att gat atg tgg tcc tgt gga tgc atc 576
Ser Thr Glu Tyr Ser Thr Pro Ile Asp Met Trp Ser Cys Gly Cys Ile
180 185 190

agg tgt tgc atg ttt gag gaa ctg aag aca gcc cag act gaa tat ctg 624
Arg Cys Cys Met Phe Glu Glu Leu Lys Thr Ala Gln Thr Glu Tyr Leu
195 200 205

aat gga aat ggg gta ccg gag cag ctg gac tca tca agc tgg aaa tcc 672
Asn Gly Asn Gly Val Pro Glu Gln Leu Asp Ser Ser Ser Trp Lys Ser
210 215 220

atg caa caa atg cca gga att aag aaa gag gca ctg aaa agg gaa aaa 720
Met Gln Gln Met Pro Gly Ile Lys Lys Glu Ala Leu Lys Arg Glu Lys
225 230 235 240

gaa aaa tcc aca aaa ctg aac act ctg gaa tgc aca cat ttc agc cca 768
Glu Lys Ser Thr Lys Leu Asn Thr Leu Glu Cys Thr His Phe Ser Pro
245 250 255

gct ctc cgt aga tgt gtg cag tgc att gca caa agc ttt ctg cag act 816
Ala Leu Arg Arg Cys Val Gln Cys Ile Ala Gln Ser Phe Leu Gln Thr
260 265 270

aga aaa tcc atg ttt gtg gaa cat 840
Arg Lys Ser Met Phe Val Glu His
275 280

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<211> 280

<212> PRT

<213> Homo sapiens

<400> 10

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20 25 30
Lys Glu Ile Arg Leu Glu His Glu Glu Gly Ala Pro Cys Thr Ala Ile
35 40 45
Arg Glu Val Ser Leu Leu Lys Asn Leu Lys His Ala Asn Ile Val Thr
50 55 60
Leu His Asp Leu Ile His Thr Asp Arg Ser Leu Thr Leu Val Phe Glu
65 70 75 80
Tyr Leu Val Arg Asp Ser Asp Leu Lys Gln Tyr Leu Asp His Cys Gly
85 90 95
Asn Leu Met Ser Met His Asn Val Lys Ile Phe Met Phe Gln Leu Leu
100 105 110

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23/155

Arg Gly Leu Ala Tyr Cys His His Arg Lys Ile Leu His Arg Glu Leu
 115 120 125
 Lys Pro Gln Asn Leu Leu Ile Asn Glu Arg Gly Glu Leu Lys Leu Ala
 130 135 140
 Asp Phe Gly Leu Ala Arg Ala Lys Ser Val Pro Thr Lys Thr Tyr Ser
 145 150 155 160
 Asn Glu Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Val Leu Leu Gly
 165 170 175
 Ser Thr Glu Tyr Ser Thr Pro Ile Asp Met Trp Ser Cys Gly Cys Ile
 180 185 190
 Arg Cys Cys Met Phe Glu Glu Leu Lys Thr Ala Gln Thr Glu Tyr Leu
 195 200 205
 Asn Gly Asn Gly Val Pro Glu Gln Leu Asp Ser Ser Ser Trp Lys Ser
 210 215 220
 Met Gln Gln Met Pro Gly Ile Lys Lys Glu Ala Leu Lys Arg Glu Lys
 225 230 235 240
 Glu Lys Ser Thr Lys Leu Asn Thr Leu Glu Cys Thr His Phe Ser Pro
 245 250 255
 Ala Leu Arg Arg Cys Val Gln Cys Ile Ala Gln Ser Phe Leu Gln Thr
 260 265 270
 Arg Lys Ser Met Phe Val Glu His
 275 280

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 <223> MOOSE03219

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 Thr Glu Gly Val Gly Pro Gly Val Pro Gly Glu Val Glu Met Val Lys
 20 25 30
 ggg cag ccg ttc gac gtg ggc ccg cgc tac acg cag cca cag cag cag 144
 Gly Gln Pro Phe Asp Val Gly Pro Arg Tyr Thr Gln Pro Gln Gln Gln
 35 40 45
 cct ctc tcc ggt ccc ctc agc tcg gcc tat gac cac gtg cgc aag act 192
 Pro Leu Ser Gly Pro Leu Ser Ser Ala Tyr Asp His Val Arg Lys Thr
 50 55 60
 cgc gtg gcc atc aag aag atc agc ccc ttc gaa cat cag acc tac tgc 240
 Arg Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys
 65 70 75 80
 cag cgc acg ctc cgg gag atc cag atc ctg ctg cgc ttc cgc cat gag 288
 Gln Arg Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe Arg His Glu
 85 90 95
 aat gtc atc ggc atc cga gac att ctg cgg gcg tcc acc ctg gaa gcc 336
 Asn Val Ile Gly Ile Arg Asp Ile Leu Arg Ala Ser Thr Leu Glu Ala
 100 105 110

24/155

atg	aga	gat	gtc	tac	att	gtg	cag	gac	ctg	atg	gag	act	gac	ctg	tac	384
Met	Arg	Asp	Val	Tyr	Ile	Val	Gln	Asp	Leu	Met	Glu	Thr	Asp	Leu	Tyr	
		115					120					125				
aag	ttg	ctg	aaa	agc	cag	cag	ctg	agc	aat	gac	cat	atc	tgc	tac	ttc	432
Lys	Leu	Leu	Lys	Ser	Gln	Gln	Leu	Ser	Asn	Asp	His	Ile	Cys	Tyr	Phe	
	130					135					140					
ctc	tac	cag	atc	ctg	cgg	ggc	ctc	aag	tac	atc	cac	tcc	gcc	aac	gtg	480
Leu	Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	Asn	Val	
145					150					155					160	
ctc	cac	cga	gat	cta	aag	ccc	tcc	aac	ctg	ctc	atc	aac	acc	acc	tgc	528
Leu	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Leu	Ile	Asn	Thr	Thr	Cys	
				165					170						175	
gac	ctt	aag	att	tgt	gat	ttc	ggc	ctg	gcc	cgg	att	gcc	gat	cct	gag	576
Asp	Leu	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Ile	Ala	Asp	Pro	Glu	
			180					185					190			
cat	gac	cac	acc	ggc	ttc	ctg	acg	gag	tat	gtg	gct	acg	cgc	tgg	tac	624
His	Asp	His	Thr	Gly	Phe	Leu	Thr	Glu	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	
		195					200					205				
cgg	gcc	cca	gag	atc	atg	ctg	aac	tcc	aag	ggc	tat	acc	aag	tcc	atc	672
Arg	Ala	Pro	Glu	Ile	Met	Leu	Asn	Ser	Lys	Gly	Tyr	Thr	Lys	Ser	Ile	
	210					215					220					
gac	atc	tgg	tct	gtg	ggc	tgc	att	ctg	gct	gag	atg	ctc	tct	aac	cgg	720
Asp	Ile	Trp	Ser	Val	Gly	Cys	Ile	Leu	Ala	Glu	Met	Leu	Ser	Asn	Arg	
225					230					235					240	
ccc	atc	ttc	cct	ggc	aag	cac	tac	ctg	gat	cag	ctc	aac	cac	att	ctg	768
Pro	Ile	Phe	Pro	Gly	Lys	His	Tyr	Leu	Asp	Gln	Leu	Asn	His	Ile	Leu	
				245					250					255		
ggc	atc	ctg	ggc	tcc	cca	tcc	cag	gag	gac	ctg	aat	tgt	atc	atc	aac	816
Gly	Ile	Leu	Gly	Ser	Pro	Ser	Gln	Glu	Asp	Leu	Asn	Cys	Ile	Ile	Asn	
			260					265					270			
atg	aag	gcc	cga	aac	tac	cta	cag	tct	ctg	ccc	tcc	aag	acc	aag	gtg	864
Met	Lys	Ala	Arg	Asn	Tyr	Leu	Gln	Ser	Leu	Pro	Ser	Lys	Thr	Lys	Val	
		275					280					285				
gct	tgg	gcc	aag	ctt	ttc	ccc	aag	tca	gac	tcc	aaa	gcc	ctt	gac	ctg	912
Ala	Trp	Ala	Lys	Leu	Phe	Pro	Lys	Ser	Asp	Ser	Lys	Ala	Leu	Asp	Leu	
	290					295					300					
ctg	gac	cgg	atg	tta	acc	ttt	aac	ccc	aat	aaa	cgg	atc	aca	gtg	gag	960
Leu	Asp	Arg	Met	Leu	Thr	Phe	Asn	Pro	Asn	Lys	Arg	Ile	Thr	Val	Glu	
305					310					315					320	
gaa	gcg	ctg	gct	cac	ccc	tac	ctg	gag	cag	tac	tat	gac	ccg	acg	gat	1008
Glu	Ala	Leu	Ala	His	Pro	Tyr	Leu	Glu	Gln	Tyr	Tyr	Asp	Pro	Thr	Asp	
				325					330					335		
gag	cca	gtg	gcc	gag	gag	ccc	ttc	acc	ttc	gcc	atg	gag	ctg	gat	gac	1056
Glu	Pro	Val	Ala	Glu	Glu	Pro	Phe	Thr	Phe	Ala	Met	Glu	Leu	Asp	Asp	
			340					345					350			

25/155

cta cct aag gag cgg ctg aag gag ctc atc ttc cag gag aca gca cgc 1104
 Leu Pro Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg
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ttc cag ccc gga gtg ctg gag 1125
 Phe Gln Pro Gly Val Leu Glu
 370 375

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 <211> 375
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Pro Leu Ser Gly Pro Leu Ser Ser Ala Tyr Asp His Val Arg Lys Thr
 50 55 60
 Arg Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr Cys
 65 70 75 80
 Gln Arg Thr Leu Arg Glu Ile Gln Ile Leu Leu Arg Phe Arg His Glu
 85 90 95
 Asn Val Ile Gly Ile Arg Asp Ile Leu Arg Ala Ser Thr Leu Glu Ala
 100 105 110
 Met Arg Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu Tyr
 115 120 125
 Lys Leu Leu Lys Ser Gln Gln Leu Ser Asn Asp His Ile Cys Tyr Phe
 130 135 140
 Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val
 145 150 155 160
 Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Ile Asn Thr Thr Cys
 165 170 175
 Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Ile Ala Asp Pro Glu
 180 185 190
 His Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp Tyr
 195 200 205
 Arg Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser Ile
 210 215 220
 Asp Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn Arg
 225 230 235 240
 Pro Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile Leu
 245 250 255
 Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile Asn
 260 265 270
 Met Lys Ala Arg Asn Tyr Leu Gln Ser Leu Pro Ser Lys Thr Lys Val
 275 280 285
 Ala Trp Ala Lys Leu Phe Pro Lys Ser Asp Ser Lys Ala Leu Asp Leu
 290 295 300
 Leu Asp Arg Met Leu Thr Phe Asn Pro Asn Lys Arg Ile Thr Val Glu
 305 310 315 320
 Glu Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Thr Asp
 325 330 335
 Glu Pro Val Ala Glu Glu Pro Phe Thr Phe Ala Met Glu Leu Asp Asp
 340 345 350
 Leu Pro Lys Glu Arg Leu Lys Glu Leu Ile Phe Gln Glu Thr Ala Arg
 355 360 365

26/155

Phe Gln Pro Gly Val Leu Glu
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<213> Homo sapiens

<220>
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<222> (1)...(1296)
<223> MOOSE03288

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Leu Gly Lys Gly Thr Phe Gly Glu Val Ala Lys Gly Trp Arg Arg Ser
20 25 30

acg ggc gag atg gtg gcc atc aag atc ctc aag aat gac gcc tac cgc 144
Thr Gly Glu Met Val Ala Ile Lys Ile Leu Lys Asn Asp Ala Tyr Arg
35 40 45

aac cgc atc atc aag aac gag ctg aag ctg ctg cac tgc atg cga ggc 192
Asn Arg Ile Ile Lys Asn Glu Leu Lys Leu Leu His Cys Met Arg Gly
50 55 60

cta gac cct gaa gag gcc cac gtc atc cgc ttc ctt gag ttc ttc cat 240
Leu Asp Pro Glu Glu Ala His Val Ile Arg Phe Leu Glu Phe Phe His
65 70 75 80

gac gcc ctc aag ttc tac ctg gtc ttt gag ctg ctg gag caa aac ctt 288
Asp Ala Leu Lys Phe Tyr Leu Val Phe Glu Leu Leu Glu Gln Asn Leu
85 90 95

ttc gag ttc cag aag gag aac aac ttc gcg ccc ctc ccc gcc cgc cac 336
Phe Glu Phe Gln Lys Glu Asn Asn Phe Ala Pro Leu Pro Ala Arg His
100 105 110

atc cgt aca gtc acc ctg cag gtg ctc aca gcc ctg gcc cgg ctc aag 384
Ile Arg Thr Val Thr Leu Gln Val Leu Thr Ala Leu Ala Arg Leu Lys
115 120 125

gag ctg gct atc atc cac gct gat ctc aag cct gag aac atc atg ctg 432
Glu Leu Ala Ile Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu
130 135 140

gtg gac cag acc cgc tgc ccc ttc agg gtg att gac ttc gga tcc gcc 480
Val Asp Gln Thr Arg Cys Pro Phe Arg Val Ile Asp Phe Gly Ser Ala
145 150 155 160

agc att ttc agc gag gtg cgc tac gtg aag gag cca tac atc cag tcg 528
Ser Ile Phe Ser Glu Val Arg Tyr Val Lys Glu Pro Tyr Ile Gln Ser
165 170 175

cgc ttc tac cgg gcc cct gag atc ctg ctg ggg ctg ccc ttc tgc gag 576
Arg Phe Tyr Arg Ala Pro Glu Ile Leu Leu Gly Leu Pro Phe Cys Glu
180 185 190

27/155

aag	gtg	gac	gtg	tgg	tcc	ctg	ggc	tgc	gtc	atg	gct	gag	ctg	cac	ctg	624
Lys	Val	Asp	Val	Trp	Ser	Leu	Gly	Cys	Val	Met	Ala	Glu	Leu	His	Leu	
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ggc	tgg	cct	ctc	tac	ccc	ggc	aac	aac	gag	tac	gac	cag	gtg	cgc	tac	672
Gly	Trp	Pro	Leu	Tyr	Pro	Gly	Asn	Asn	Glu	Tyr	Asp	Gln	Val	Arg	Tyr	
	210					215					220					
atc	tgc	gaa	acc	cag	ggc	ctg	ccc	aag	cca	cac	ctg	ttg	cac	gcc	gcc	720
Ile	Cys	Glu	Thr	Gln	Gly	Leu	Pro	Lys	Pro	His	Leu	Leu	His	Ala	Ala	
225					230					235					240	
tgc	aag	gcc	cac	cac	ttc	ttc	aag	cgc	aac	ccc	cac	cct	gac	gct	gcc	768
Cys	Lys	Ala	His	His	Phe	Phe	Lys	Arg	Asn	Pro	His	Pro	Asp	Ala	Ala	
				245					250					255		
aac	ccc	tgg	cag	ctc	aat	cgg	cta	acc	ttc	cct	gac	cgg	gag	gcg	ctg	816
Asn	Pro	Trp	Gln	Leu	Asn	Arg	Leu	Thr	Phe	Pro	Asp	Arg	Glu	Ala	Leu	
			260					265					270			
gcg	gag	cac	gcc	gac	ctc	aag	agc	atg	gtg	gag	ctg	atc	aag	cgc	atg	864
Ala	Glu	His	Ala	Asp	Leu	Lys	Ser	Met	Val	Glu	Leu	Ile	Lys	Arg	Met	
		275					280					285				
ctg	acc	tgg	gag	tca	cac	gaa	cgc	atc	agc	ccc	agt	gct	gcc	ctg	cgc	912
Leu	Thr	Trp	Glu	Ser	His	Glu	Arg	Ile	Ser	Pro	Ser	Ala	Ala	Leu	Arg	
	290					295					300					
cac	ccc	ttc	gtg	tcc	atg	cag	cag	ctg	cgc	agt	gcc	cac	gag	acc	acc	960
His	Pro	Phe	Val	Ser	Met	Gln	Gln	Leu	Arg	Ser	Ala	His	Glu	Thr	Thr	
305					310					315					320	
cac	tac	tac	cag	ctc	tcg	ctg	cgc	agc	tac	cgc	ctc	tcg	ctg	caa	gtg	1008
His	Tyr	Tyr	Gln	Leu	Ser	Leu	Arg	Ser	Tyr	Arg	Leu	Ser	Leu	Gln	Val	
				325					330					335		
gag	ggg	aag	ccc	ccc	acg	ccc	gtc	gtg	gcc	gca	gaa	gat	ggg	acc	ccc	1056
Glu	Gly	Lys	Pro	Pro	Thr	Pro	Val	Val	Ala	Ala	Glu	Asp	Gly	Thr	Pro	
			340				345						350			
tac	tac	tgt	ctg	gct	gag	gag	aag	gag	gct	gcg	gcc	cct	cat	cct	gtt	1104
Tyr	Tyr	Cys	Leu	Ala	Glu	Glu	Lys	Glu	Ala	Ala	Ala	Pro	His	Pro	Val	
		355					360					365				
tcc	agc	cca	tgc	ctc	cta	cct	ccc	caa	atc	cca	cat	cct	gca	ccc	ctg	1152
Ser	Ser	Pro	Cys	Leu	Leu	Pro	Pro	Gln	Ile	Pro	His	Pro	Ala	Pro	Leu	
	370					375					380					
cct	cag	gct	tcc	tgc	cct	caa	ccc	caa	tat	tct	gag	cct	tct	ctt	ttt	1200
Pro	Gln	Ala	Ser	Cys	Pro	Gln	Pro	Gln	Tyr	Ser	Glu	Pro	Ser	Leu	Phe	
385					390					395					400	
ttt	tgt	tgt	ttt	ttt	gag	aca	gaa	caa	act	gct	atg	aat	att	ctt	gta	1248
Phe	Cys	Cys	Phe	Phe	Glu	Thr	Glu	Gln	Thr	Ala	Met	Asn	Ile	Leu	Val	
				405					410					415		
cgt	gtc	tcc	tgg	tgt	gtg	caa	caa	gcc	aca	tct	cat	cga	ttc	caa	gac	1296
Arg	Val	Ser	Trp	Cys	Val	Gln	Gln	Ala	Thr	Ser	His	Arg	Phe	Gln	Asp	
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28/155

<210> 14

<211> 432

<212> PRT

<213> Homo sapiens

<400> 14

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Thr Gly Glu Met Val Ala Ile Lys Ile Leu Lys Asn Asp Ala Tyr Arg
      35      40      45
Asn Arg Ile Ile Lys Asn Glu Leu Lys Leu Leu His Cys Met Arg Gly
      50      55      60
Leu Asp Pro Glu Glu Ala His Val Ile Arg Phe Leu Glu Phe Phe His
      65      70      75      80
Asp Ala Leu Lys Phe Tyr Leu Val Phe Glu Leu Leu Glu Gln Asn Leu
      85      90      95
Phe Glu Phe Gln Lys Glu Asn Asn Phe Ala Pro Leu Pro Ala Arg His
      100      105      110
Ile Arg Thr Val Thr Leu Gln Val Leu Thr Ala Leu Ala Arg Leu Lys
      115      120      125
Glu Leu Ala Ile Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu
      130      135      140
Val Asp Gln Thr Arg Cys Pro Phe Arg Val Ile Asp Phe Gly Ser Ala
      145      150      155      160
Ser Ile Phe Ser Glu Val Arg Tyr Val Lys Glu Pro Tyr Ile Gln Ser
      165      170      175
Arg Phe Tyr Arg Ala Pro Glu Ile Leu Leu Gly Leu Pro Phe Cys Glu
      180      185      190
Lys Val Asp Val Trp Ser Leu Gly Cys Val Met Ala Glu Leu His Leu
      195      200      205
Gly Trp Pro Leu Tyr Pro Gly Asn Asn Glu Tyr Asp Gln Val Arg Tyr
      210      215      220
Ile Cys Glu Thr Gln Gly Leu Pro Lys Pro His Leu Leu His Ala Ala
      225      230      235      240
Cys Lys Ala His His Phe Phe Lys Arg Asn Pro His Pro Asp Ala Ala
      245      250      255
Asn Pro Trp Gln Leu Asn Arg Leu Thr Phe Pro Asp Arg Glu Ala Leu
      260      265      270
Ala Glu His Ala Asp Leu Lys Ser Met Val Glu Leu Ile Lys Arg Met
      275      280      285
Leu Thr Trp Glu Ser His Glu Arg Ile Ser Pro Ser Ala Ala Leu Arg
      290      295      300
His Pro Phe Val Ser Met Gln Gln Leu Arg Ser Ala His Glu Thr Thr
      305      310      315      320
His Tyr Tyr Gln Leu Ser Leu Arg Ser Tyr Arg Leu Ser Leu Gln Val
      325      330      335
Glu Gly Lys Pro Pro Thr Pro Val Val Ala Ala Glu Asp Gly Thr Pro
      340      345      350
Tyr Tyr Cys Leu Ala Glu Glu Lys Glu Ala Ala Ala Pro His Pro Val
      355      360      365
Ser Ser Pro Cys Leu Leu Pro Pro Gln Ile Pro His Pro Ala Pro Leu
      370      375      380
Pro Gln Ala Ser Cys Pro Gln Pro Gln Tyr Ser Glu Pro Ser Leu Phe
      385      390      395      400
Phe Cys Cys Phe Phe Glu Thr Glu Gln Thr Ala Met Asn Ile Leu Val
      405      410      415
Arg Val Ser Trp Cys Val Gln Gln Ala Thr Ser His Arg Phe Gln Asp
      420      425      430

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29/155

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 <211> 1383
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> MOOSE03296

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 Gln Arg Arg Gly Ile Arg Thr Lys Arg Met Lys Leu Lys Cys Ser Gln
 20 25 30

cac aaa aaa atg ata aat gtt gac aaa aaa aaa aaa tcc agg aaa 144
 His Lys Lys Met Ile Asn Val Asp Lys Lys Lys Lys Lys Ser Arg Lys
 35 40 45

aaa aat cac cag aaa cta gaa cgt gag gct cgg ata tgt cga ctt ctg 192
 Lys Asn His Gln Lys Leu Glu Arg Glu Ala Arg Ile Cys Arg Leu Leu
 50 55 60

aaa cat cca aac atc gtg cgc ctc cat gac agt att tct gaa gaa ggg 240
 Lys His Pro Asn Ile Val Arg Leu His Asp Ser Ile Ser Glu Glu Gly
 65 70 75 80

ttt cac tac ctc gtg ttt gac ctt gtt acc ggc ggg gag ctg ttt gaa 288
 Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly Glu Leu Phe Glu
 85 90 95

gac att gtg gcc aga gag tac tac agt gaa gca gat gcc agc cac tgt 336
 Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys
 100 105 110

ata cat cag att ctg gag agt gtt aac cac atc cac cag cat gac atc 384
 Ile His Gln Ile Leu Glu Ser Val Asn His Ile His Gln His Asp Ile
 115 120 125

gtc cac agg gac ctg aag cct gag aac ctg ctg ctg gcg agt aaa tgc 432
 Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Cys
 130 135 140

aag ggt gcc gcc gtc aag ctg gct gat ttt ggc cta gcc atc gaa gta 480
 Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val
 145 150 155 160

cag gga gag cag cag gct tgg ttt ggt aag ggt ttt gct ggc acc cca 528
 Gln Gly Glu Gln Gln Ala Trp Phe Gly Lys Gly Phe Ala Gly Thr Pro
 165 170 175

ggt tac ttg tcc cct gag gtc ttg agg aaa gat ccc tat gga aaa cct 576
 Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Asp Pro Tyr Gly Lys Pro
 180 185 190

gtg gat atc tgg gcc tgc ggg gtc atc ctg tat atc ctc ctg gtg ggc 624
 Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu Val Gly
 195 200 205

30/155

tat	cct	ccc	ttc	tgg	gat	gag	gat	cag	cac	aag	ctg	tat	cag	cag	atc	672
Tyr	Pro	Pro	Phe	Trp	Asp	Glu	Asp	Gln	His	Lys	Leu	Tyr	Gln	Gln	Ile	
	210					215					220					
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Lys	Ala	Gly	Ala	Tyr	Asp	Phe	Pro	Ser	Pro	Glu	Trp	Asp	Thr	Val	Thr	
225					230					235					240	
cct	gaa	gcc	aag	aac	ttg	atc	aac	cag	atg	ctg	acc	ata	aac	cca	gca	768
Pro	Glu	Ala	Lys	Asn	Leu	Ile	Asn	Gln	Met	Leu	Thr	Ile	Asn	Pro	Ala	
				245					250					255		
aag	cgc	atc	acg	gct	gac	cag	gct	ctc	aag	cac	ccg	tgg	gtc	tgt	caa	816
Lys	Arg	Ile	Thr	Ala	Asp	Gln	Ala	Leu	Lys	His	Pro	Trp	Val	Cys	Gln	
			260					265					270			
cga	tcc	acg	gtg	gca	tcc	atg	atg	cat	cgt	cag	gag	act	gtg	gag	tgt	864
Arg	Ser	Thr	Val	Ala	Ser	Met	Met	His	Arg	Gln	Glu	Thr	Val	Glu	Cys	
			275				280					285				
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Leu	Arg	Lys	Phe	Asn	Ala	Arg	Arg	Lys	Leu	Lys	Gly	Ala	Ile	Leu	Thr	
	290					295					300					
acc	atg	ctt	gtc	tcc	agg	aac	ttc	tca	ggg	att	cgg	aag	ggg	aat	ctt	960
Thr	Met	Leu	Val	Ser	Arg	Asn	Phe	Ser	Gly	Ile	Arg	Lys	Gly	Asn	Leu	
305					310					315					320	
cat	ctt	ctc	tca	cag	gag	cca	caa	acc	act	gtg	gta	cac	aac	gct	aca	1008
His	Leu	Leu	Ser	Gln	Glu	Pro	Gln	Thr	Thr	Val	Val	His	Asn	Ala	Thr	
				325					330					335		
gat	ggg	atc	aag	ggc	tcc	aca	gag	agc	tgc	aac	acc	acc	aca	gaa	gat	1056
Asp	Gly	Ile	Lys	Gly	Ser	Thr	Glu	Ser	Cys	Asn	Thr	Thr	Thr	Glu	Asp	
			340					345					350			
gag	gac	ctc	aaa	gtg	cga	aaa	cag	gag	atc	att	aag	att	aca	gaa	cag	1104
Glu	Asp	Leu	Lys	Val	Arg	Lys	Gln	Glu	Ile	Ile	Lys	Ile	Thr	Glu	Gln	
		355					360					365				
ctg	att	gaa	gcc	atc	aac	aat	ggg	gac	ttt	gag	gcc	tac	acg	aag	att	1152
Leu	Ile	Glu	Ala	Ile	Asn	Asn	Gly	Asp	Phe	Glu	Ala	Tyr	Thr	Lys	Ile	
	370					375					380					
tgt	gat	cca	ggc	ctc	act	tcc	ttt	gag	cct	gag	gcc	ctt	ggg	aac	ctc	1200
Cys	Asp	Pro	Gly	Leu	Thr	Ser	Phe	Glu	Pro	Glu	Ala	Leu	Gly	Asn	Leu	
385					390					395				400		
gtg	gag	ggg	atg	gat	ttc	cat	aag	ttt	tac	ttt	gag	aat	ctc	ctg	tcc	1248
Val	Glu	Gly	Met	Asp	Phe	His	Lys	Phe	Tyr	Phe	Glu	Asn	Leu	Leu	Ser	
				405					410					415		
aag	aac	agc	aag	cct	atc	cat	acc	acc	atc	cta	aac	cca	cac	gtc	cac	1296
Lys	Asn	Ser	Lys	Pro	Ile	His	Thr	Thr	Ile	Leu	Asn	Pro	His	Val	His	
			420					425					430			
gtg	att	ggg	gag	gac	gca	gcg	tgc	atc	gcc	tac	atc	cgc	ctc	acc	cag	1344
Val	Ile	Gly	Glu	Asp	Ala	Ala	Cys	Ile	Ala	Tyr	Ile	Arg	Leu	Thr	Gln	
		435					440					445				

31/155

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 Tyr Ile Asp Gly Gln Gly Arg Pro Arg Thr Ser Gln Ser
 450 455 460

1383

<210> 16
 <211> 461
 <212> PRT
 <213> Homo sapiens

<400> 16
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 Gln Arg Arg Gly Ile Arg Thr Lys Arg Met Lys Leu Lys Cys Ser Gln
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 His Lys Lys Met Ile Asn Val Asp Lys Lys Lys Lys Lys Ser Arg Lys
 35 40 45
 Lys Asn His Gln Lys Leu Glu Arg Glu Ala Arg Ile Cys Arg Leu Leu
 50 55 60
 Lys His Pro Asn Ile Val Arg Leu His Asp Ser Ile Ser Glu Glu Gly
 65 70 75 80
 Phe His Tyr Leu Val Phe Asp Leu Val Thr Gly Gly Glu Leu Phe Glu
 85 90 95
 Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys
 100 105 110
 Ile His Gln Ile Leu Glu Ser Val Asn His Ile His Gln His Asp Ile
 115 120 125
 Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Cys
 130 135 140
 Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val
 145 150 155 160
 Gln Gly Glu Gln Gln Ala Trp Phe Gly Lys Gly Phe Ala Gly Thr Pro
 165 170 175
 Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Asp Pro Tyr Gly Lys Pro
 180 185 190
 Val Asp Ile Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu Val Gly
 195 200 205
 Tyr Pro Pro Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln Gln Ile
 210 215 220
 Lys Ala Gly Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr Val Thr
 225 230 235 240
 Pro Glu Ala Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn Pro Ala
 245 250 255
 Lys Arg Ile Thr Ala Asp Gln Ala Leu Lys His Pro Trp Val Cys Gln
 260 265 270
 Arg Ser Thr Val Ala Ser Met Met His Arg Gln Glu Thr Val Glu Cys
 275 280 285
 Leu Arg Lys Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile Leu Thr
 290 295 300
 Thr Met Leu Val Ser Arg Asn Phe Ser Gly Ile Arg Lys Gly Asn Leu
 305 310 315 320
 His Leu Leu Ser Gln Glu Pro Gln Thr Thr Val Val His Asn Ala Thr
 325 330 335
 Asp Gly Ile Lys Gly Ser Thr Glu Ser Cys Asn Thr Thr Thr Glu Asp
 340 345 350
 Glu Asp Leu Lys Val Arg Lys Gln Glu Ile Ile Lys Ile Thr Glu Gln
 355 360 365
 Leu Ile Glu Ala Ile Asn Asn Gly Asp Phe Glu Ala Tyr Thr Lys Ile
 370 375 380
 Cys Asp Pro Gly Leu Thr Ser Phe Glu Pro Glu Ala Leu Gly Asn Leu
 385 390 395 400

32/155

Val	Glu	Gly	Met	Asp	Phe	His	Lys	Phe	Tyr	Phe	Glu	Asn	Leu	Leu	Ser	
				405					410					415		
Lys	Asn	Ser	Lys	Pro	Ile	His	Thr	Thr	Ile	Leu	Asn	Pro	His	Val	His	
			420					425					430			
Val	Ile	Gly	Glu	Asp	Ala	Ala	Cys	Ile	Ala	Tyr	Ile	Arg	Leu	Thr	Gln	
		435					440					445				
Tyr	Ile	Asp	Gly	Gln	Gly	Arg	Pro	Arg	Thr	Ser	Gln	Ser				
	450					455					460					

<210> 17
 <211> 1107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1107)
 <223> MOOSE03301

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Ser	Leu	Thr	Leu	Leu	Ser	Gln	Glu	Glu	Gln	Leu	Val	Leu	Tyr	Arg	Phe	
1				5					10					15		
tcc aga ggg gct ttt tgg aaa tat cta gaa agg aga gag aaa ata gaa																96
Ser	Arg	Gly	Ala	Phe	Trp	Lys	Tyr	Leu	Glu	Arg	Arg	Glu	Lys	Ile	Glu	
			20					25					30			
aca aaa aaa att ttt aag tgc aaa gtt aag ctt gaa aga aaa tat cac																144
Thr	Lys	Lys	Ile	Phe	Lys	Cys	Lys	Val	Lys	Leu	Glu	Arg	Lys	Tyr	His	
		35					40					45				
cag aaa cta gaa cgt gag gct cgg ata tgt cga ctt ctg aaa cat cca																192
Gln	Lys	Leu	Glu	Arg	Glu	Ala	Arg	Ile	Cys	Arg	Leu	Leu	Lys	His	Pro	
	50					55					60					
aac atc gtg cgc ctc cat gac agt att tct gaa gaa ggg ttt cac tac																240
Asn	Ile	Val	Arg	Leu	His	Asp	Ser	Ile	Ser	Glu	Glu	Gly	Phe	His	Tyr	
	65				70					75					80	
ctc gtg ttt gac ctt gtt acc ggc ggg gag ctg ttt gaa gac att gtg																288
Leu	Val	Phe	Asp	Leu	Val	Thr	Gly	Gly	Glu	Leu	Phe	Glu	Asp	Ile	Val	
			85						90					95		
gcc aga gag tac tac agt gaa gca gat gcc agc cac tgt ata cat cag																336
Ala	Arg	Glu	Tyr	Ser	Glu	Ala	Asp	Ala	Ser	His	Cys	Ile	His	Gln		
			100				105					110				
att ctg gag agt gtt aac cac atc cac cag cat gac atc gtc cac agg																384
Ile	Leu	Glu	Ser	Val	Asn	His	Ile	His	Gln	His	Asp	Ile	Val	His	Arg	
		115					120					125				
gac ctg aag cct gag aac ctg ctg ctg gcg agt aaa tgc aag ggt gcc																432
Asp	Leu	Lys	Pro	Glu	Asn	Leu	Leu	Leu	Ala	Ser	Lys	Cys	Lys	Gly	Ala	
	130					135					140					
gcc gtc aag ctg gct gat ttt ggc cta gcc atc gaa gta cag gga gag																480
Ala	Val	Lys	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Ile	Glu	Val	Gln	Gly	Glu	
	145				150					155					160	

33/155

cag	cag	gct	tgg	ttt	ggg	aag	ggg	ttt	gct	ggc	acc	cca	ggg	tac	ttg	528
Gln	Gln	Ala	Trp	Phe	Gly	Lys	Gly	Phe	Ala	Gly	Thr	Pro	Gly	Tyr	Leu	
				165					170					175		
tcc	cct	gag	gtc	ttg	agg	aaa	gat	ccc	tat	gga	aaa	cct	gtg	gat	atc	576
Ser	Pro	Glu	Val	Leu	Arg	Lys	Asp	Pro	Tyr	Gly	Lys	Pro	Val	Asp	Ile	
			180					185					190			
tgg	gcc	tgc	ggg	gtc	atc	ctg	tat	atc	ctc	ctg	gtg	ggc	tat	cct	ccc	624
Trp	Ala	Cys	Gly	Val	Ile	Leu	Tyr	Ile	Leu	Leu	Val	Gly	Tyr	Pro	Pro	
		195					200					205				
ttc	tgg	gat	gag	gat	cag	cac	aag	ctg	tat	cag	cag	atc	aag	gct	gga	672
Phe	Trp	Asp	Glu	Asp	Gln	His	Lys	Leu	Tyr	Gln	Gln	Ile	Lys	Ala	Gly	
	210					215					220					
gcc	tat	gat	ttc	cca	tca	cca	gaa	tgg	gac	acg	gta	act	cct	gaa	gcc	720
Ala	Tyr	Asp	Phe	Pro	Ser	Pro	Glu	Trp	Asp	Thr	Val	Thr	Pro	Glu	Ala	
225					230					235					240	
aag	aac	ttg	atc	aac	cag	atg	ctg	acc	ata	aac	cca	gca	aag	cgc	atc	768
Lys	Asn	Leu	Ile	Asn	Gln	Met	Leu	Thr	Ile	Asn	Pro	Ala	Lys	Arg	Ile	
				245					250					255		
acg	gct	gac	cag	gct	ctc	aag	cac	ccg	tgg	gtc	tgt	caa	cga	tcc	acg	816
Thr	Ala	Asp	Gln	Ala	Leu	Lys	His	Pro	Trp	Val	Cys	Gln	Arg	Ser	Thr	
			260					265					270			
gtg	gca	tcc	atg	atg	cat	cgt	cag	gag	act	gtg	gag	tgt	ttg	cgc	aag	864
Val	Ala	Ser	Met	Met	His	Arg	Gln	Glu	Thr	Val	Glu	Cys	Leu	Arg	Lys	
		275					280					285				
ttc	aat	gcc	cgg	aga	aaa	ctg	aag	ggg	gcc	atc	ctc	acg	acc	atg	ctt	912
Phe	Asn	Ala	Arg	Arg	Lys	Leu	Lys	Gly	Ala	Ile	Leu	Thr	Thr	Met	Leu	
	290					295					300					
gtc	tcc	agg	aac	ttc	tca	ggg	atg	aca	gag	tct	gtc	cgg	aag	ctt	ctg	960
Val	Ser	Arg	Asn	Phe	Ser	Gly	Met	Thr	Glu	Ser	Val	Arg	Lys	Leu	Leu	
305					310					315					320	
cag	aaa	gag	gtg	tct	atg	gat	gca	atc	aag	aag	gaa	ggg	cac	ctg	tgt	1008
Gln	Lys	Glu	Val	Ser	Met	Asp	Ala	Ile	Lys	Lys	Glu	Gly	His	Leu	Cys	
				325					330					335		
gtt	tct	cta	ggg	ctg	ttt	ttt	gag	ttg	acc	tcc	aat	agg	aga	tgt	ggc	1056
Val	Ser	Leu	Gly	Leu	Phe	Phe	Glu	Leu	Thr	Ser	Asn	Arg	Arg	Cys	Gly	
			340					345					350			
tta	tcc	tgg	act	cta	gca	gaa	gct	cat	agg	aga	gag	cgt	act	gga	gaa	1104
Leu	Ser	Trp	Thr	Leu	Ala	Glu	Ala	His	Arg	Arg	Glu	Arg	Thr	Gly	Glu	
		355					360					365				
agc																1107
Ser																

<210> 18

<211> 369

<212> PRT

<213> Homo sapiens

34/155

<400> 18

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Ser Leu Thr Leu Leu Ser Gln Glu Glu Gln Leu Val Leu Tyr Arg Phe
 1           5           10           15
Ser Arg Gly Ala Phe Trp Lys Tyr Leu Glu Arg Arg Glu Lys Ile Glu
           20           25           30
Thr Lys Lys Ile Phe Lys Cys Lys Val Lys Leu Glu Arg Lys Tyr His
           35           40           45
Gln Lys Leu Glu Arg Glu Ala Arg Ile Cys Arg Leu Leu Lys His Pro
 50           55           60
Asn Ile Val Arg Leu His Asp Ser Ile Ser Glu Glu Gly Phe His Tyr
65           70           75           80
Leu Val Phe Asp Leu Val Thr Gly Gly Glu Leu Phe Glu Asp Ile Val
           85           90           95
Ala Arg Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys Ile His Gln
           100          105          110
Ile Leu Glu Ser Val Asn His Ile His Gln His Asp Ile Val His Arg
           115          120          125
Asp Leu Lys Pro Glu Asn Leu Leu Ala Ser Lys Cys Lys Gly Ala
130          135          140
Ala Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Glu
145          150          155          160
Gln Gln Ala Trp Phe Gly Lys Gly Phe Ala Gly Thr Pro Gly Tyr Leu
           165          170          175
Ser Pro Glu Val Leu Arg Lys Asp Pro Tyr Gly Lys Pro Val Asp Ile
           180          185          190
Trp Ala Cys Gly Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr Pro Pro
           195          200          205
Phe Trp Asp Glu Asp Gln His Lys Leu Tyr Gln Gln Ile Lys Ala Gly
210          215          220
Ala Tyr Asp Phe Pro Ser Pro Glu Trp Asp Thr Val Thr Pro Glu Ala
225          230          235          240
Lys Asn Leu Ile Asn Gln Met Leu Thr Ile Asn Pro Ala Lys Arg Ile
           245          250          255
Thr Ala Asp Gln Ala Leu Lys His Pro Trp Val Cys Gln Arg Ser Thr
           260          265          270
Val Ala Ser Met Met His Arg Gln Glu Thr Val Glu Cys Leu Arg Lys
           275          280          285
Phe Asn Ala Arg Arg Lys Leu Lys Gly Ala Ile Leu Thr Thr Met Leu
290          295          300
Val Ser Arg Asn Phe Ser Gly Met Thr Glu Ser Val Arg Lys Leu Leu
305          310          315          320
Gln Lys Glu Val Ser Met Asp Ala Ile Lys Lys Glu Gly His Leu Cys
           325          330          335
Val Ser Leu Gly Leu Phe Phe Glu Leu Thr Ser Asn Arg Arg Cys Gly
           340          345          350
Leu Ser Trp Thr Leu Ala Glu Ala His Arg Arg Glu Arg Thr Gly Glu
           355          360          365
Ser

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<210> 19

<211> 1086

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1086)

<223> MOOSE03304

<400> 19

35/155

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Phe Asp Pro Arg Val Thr Ala Lys Tyr Asp Ile Lys Ala Leu Ile Gly	
1 5 10 15	
cga ggc agc ttc agc cga gtg gta cgt gta gag cac cgg gca acc cgg	96
Arg Gly Ser Phe Ser Arg Val Val Arg Val Glu His Arg Ala Thr Arg	
20 25 30	
cag ccg tat gcc atc aag atg att gag acc aag tac cgg gag ggg cgg	144
Gln Pro Tyr Ala Ile Lys Met Ile Glu Thr Lys Tyr Arg Glu Gly Arg	
35 40 45	
gag gtg tgt gag tcg gag ctg cgt gtg ctg cgt cgg gtg cgt cat gcc	192
Glu Val Cys Glu Ser Glu Leu Arg Val Leu Arg Arg Val Arg His Ala	
50 55 60	
aac atc atc cag ctg gtg gag gtg ttc gag aca cag gag cgg gtg tac	240
Asn Ile Ile Gln Leu Val Glu Val Phe Glu Thr Gln Glu Arg Val Tyr	
65 70 75 80	
atg gtg atg gag ctg gcc act ggt gga gag ctc ttt gac cgc atc att	288
Met Val Met Glu Leu Ala Thr Gly Gly Glu Leu Phe Asp Arg Ile Ile	
85 90 95	
gcc aag ggc tcc ttc acc gag cgt gac gcc acg cgg gtg ctg cag atg	336
Ala Lys Gly Ser Phe Thr Glu Arg Asp Ala Thr Arg Val Leu Gln Met	
100 105 110	
gtg ctg gat ggc gtc cgg tat ctg cat gca ctg ggc atc aca cac cga	384
Val Leu Asp Gly Val Arg Tyr Leu His Ala Leu Gly Ile Thr His Arg	
115 120 125	
gac ctc aaa cct gag aat ctg ctc tac tac cat ccg ggc act gac tcc	432
Asp Leu Lys Pro Glu Asn Leu Leu Tyr Tyr His Pro Gly Thr Asp Ser	
130 135 140	
aag atc atc atc acc gac ttc ggc ctg gcc agt gct cgc aag aag ggt	480
Lys Ile Ile Ile Thr Asp Phe Gly Leu Ala Ser Ala Arg Lys Lys Gly	
145 150 155 160	
gat gac tgc ttg atg aag acc acc tgt ggc acg cct gag tac att gcc	528
Asp Asp Cys Leu Met Lys Thr Thr Cys Gly Thr Pro Glu Tyr Ile Ala	
165 170 175	
cca gaa gtc ctg gtc cgc aag cca tac acc aac tca gtg gac atg tgg	576
Pro Glu Val Leu Val Arg Lys Pro Tyr Thr Asn Ser Val Asp Met Trp	
180 185 190	
gcg ctg ggc gtc att gcc tac atc cta ctc agt ggc acc atg ccg ttt	624
Ala Leu Gly Val Ile Ala Tyr Ile Leu Leu Ser Gly Thr Met Pro Phe	
195 200 205	
gag gat gac aac cgt acc cgg ctg tac cgg cag atc ctc agg ggc aag	672
Glu Asp Asn Arg Thr Leu Tyr Arg Gln Ile Leu Arg Gly Lys	
210 215 220	
tac agt tac tct ggg gag ccc tgg cct agt gtg tcc aac ctg gcc aag	720
Tyr Ser Tyr Ser Gly Glu Pro Trp Pro Ser Val Ser Asn Leu Ala Lys	
225 230 235 240	

36/155

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gac ttc att gac cgc ctg ctg aca gtg gac cct gga gcc cgt atg act 768
Asp Phe Ile Asp Arg Leu Leu Thr Val Asp Pro Gly Ala Arg Met Thr
245 250 255

gca ctg cag gcc ctg agg cac ccg tgg gtg gtg agc atg gct gcc tct 816
Ala Leu Gln Ala Leu Arg His Pro Trp Val Val Ser Met Ala Ala Ser
260 265 270

tca tcc atg aag aac ctg cac cgc tcc ata tcc cag aac ctc ctt aaa 864
Ser Ser Met Lys Asn Leu His Arg Ser Ile Ser Gln Asn Leu Leu Lys
275 280 285

cgt gcc tcc tcg cgc tgc cag agc acc aaa tct gcc cag tcc acg cgt 912
Arg Ala Ser Ser Arg Cys Gln Ser Thr Lys Ser Ala Gln Ser Thr Arg
290 295 300

tcc agc cgc tcc aca cgc tcc aat aag tca cgc cgt cag ggg ccc agc 960
Ser Ser Arg Ser Thr Arg Ser Asn Lys Ser Arg Arg Gln Gly Pro Ser
305 310 315 320

aaa ggt ttg ttg gag aaa cgt gtc atc tct ccc cat gtg agt cct gtg 1008
Lys Gly Leu Leu Glu Lys Arg Val Ile Ser Pro His Val Ser Pro Val
325 330 335

acc ctt att agc ctg gaa aac ttg gag tca caa gcc cag cat gtg cag 1056
Thr Leu Ile Ser Leu Glu Asn Leu Glu Ser Gln Ala Gln His Val Gln
340 345 350

aca gaa gac gag ctt cac gtg agc agt gca 1086
Thr Glu Asp Glu Leu His Val Ser Ser Ala
355 360

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<210> 20
 <211> 362
 <212> PRT
 <213> Homo sapiens

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<400> 20
Phe Asp Pro Arg Val Thr Ala Lys Tyr Asp Ile Lys Ala Leu Ile Gly
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20 25 30
Gln Pro Tyr Ala Ile Lys Met Ile Glu Thr Lys Tyr Arg Glu Gly Arg
35 40 45
Glu Val Cys Glu Ser Glu Leu Arg Val Leu Arg Arg Val Arg His Ala
50 55 60
Asn Ile Ile Gln Leu Val Glu Val Phe Glu Thr Gln Glu Arg Val Tyr
65 70 75 80
Met Val Met Glu Leu Ala Thr Gly Gly Glu Leu Phe Asp Arg Ile Ile
85 90 95
Ala Lys Gly Ser Phe Thr Glu Arg Asp Ala Thr Arg Val Leu Gln Met
100 105 110
Val Leu Asp Gly Val Arg Tyr Leu His Ala Leu Gly Ile Thr His Arg
115 120 125
Asp Leu Lys Pro Glu Asn Leu Leu Tyr Tyr His Pro Gly Thr Asp Ser
130 135 140
Lys Ile Ile Ile Thr Asp Phe Gly Leu Ala Ser Ala Arg Lys Lys Gly
145 150 155 160
Asp Asp Cys Leu Met Lys Thr Thr Cys Gly Thr Pro Glu Tyr Ile Ala
165 170 175

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37/155

Pro Glu Val Leu Val Arg Lys Pro Tyr Thr Asn Ser Val Asp Met Trp
180 185 190
Ala Leu Gly Val Ile Ala Tyr Ile Leu Leu Ser Gly Thr Met Pro Phe
195 200 205
Glu Asp Asp Asn Arg Thr Arg Leu Tyr Arg Gln Ile Leu Arg Gly Lys
210 215 220
Tyr Ser Tyr Ser Gly Glu Pro Trp Pro Ser Val Ser Asn Leu Ala Lys
225 230 235 240
Asp Phe Ile Asp Arg Leu Leu Thr Val Asp Pro Gly Ala Arg Met Thr
245 250 255
Ala Leu Gln Ala Leu Arg His Pro Trp Val Val Ser Met Ala Ala Ser
260 265 270
Ser Ser Met Lys Asn Leu His Arg Ser Ile Ser Gln Asn Leu Leu Lys
275 280 285
Arg Ala Ser Ser Arg Cys Gln Ser Thr Lys Ser Ala Gln Ser Thr Arg
290 295 300
Ser Ser Arg Ser Thr Arg Ser Asn Lys Ser Arg Arg Gln Gly Pro Ser
305 310 315 320
Lys Gly Leu Leu Glu Lys Arg Val Ile Ser Pro His Val Ser Pro Val
325 330 335
Thr Leu Ile Ser Leu Glu Asn Leu Glu Ser Gln Ala Gln His Val Gln
340 345 350
Thr Glu Asp Glu Leu His Val Ser Ser Ala
355 360

<210> 21
<211> 1092
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)... (1092)
<223> MOOSE03306

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aca tgt ttg gtt ttt ctt ccc aac aga tat gac atc aaa gct ctt att 48
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ggg aca ggc agt ttc agc agg gtt gtc agg gta gag cag aag acc acc 96
Gly Thr Gly Ser Phe Ser Arg Val Val Arg Val Glu Gln Lys Thr Thr
20 25 30

aag aaa cct ttt gca ata aaa gtg atg gaa acc aga gag agg gaa ggt 144
Lys Lys Pro Phe Ala Ile Lys Val Met Glu Thr Arg Glu Arg Glu Gly
35 40 45

aga gaa gcg tgc gtg tct gag ctg agc gtc ctg cgg cgg gtt agc cat 192
Arg Glu Ala Cys Val Ser Glu Leu Ser Val Leu Arg Arg Val Ser His
50 55 60

cgt tac att gtc cag ctc atg gag atc ttt gag act gag gat caa gtt 240
Arg Tyr Ile Val Gln Leu Met Glu Ile Phe Glu Thr Glu Asp Gln Val
65 70 75 80

tac atg gta atg gag ctg gct acc gga ggg gag ctc ttt gat cga ctc 288
Tyr Met Val Met Glu Leu Ala Thr Gly Gly Glu Leu Phe Asp Arg Leu
85 90 95

38/155

att gct cag gga tcc ttt aca gag cgg gat gcc gtc agg atc ctc cag	336
Ile Ala Gln Gly Ser Phe Thr Glu Arg Asp Ala Val Arg Ile Leu Gln	
100 105 110	
atg gtt gct gat ggg att agg tat ttg cat gcg ctg cag ata act cat	384
Met Val Ala Asp Gly Ile Arg Tyr Leu His Ala Leu Gln Ile Thr His	
115 120 125	
agg aat cta aag cct gaa aac ctc tta tac tat cat cca ggt gaa gag	432
Arg Asn Leu Lys Pro Glu Asn Leu Leu Tyr Tyr His Pro Gly Glu Glu	
130 135 140	
tcg aaa att tta att aca gat ttt ggt ttg gca tac tcc ggg aaa aaa	480
Ser Lys Ile Leu Ile Thr Asp Phe Gly Leu Ala Tyr Ser Gly Lys Lys	
145 150 155 160	
agt ggt gac tgg aca atg aag aca ctc tgt ggg acc cca gag tac ata	528
Ser Gly Asp Trp Thr Met Lys Thr Leu Cys Gly Thr Pro Glu Tyr Ile	
165 170 175	
gct cct gag gtt ttg cta agg aag cct tat acc agt gca gtg gac atg	576
Ala Pro Glu Val Leu Leu Arg Lys Pro Tyr Thr Ser Ala Val Asp Met	
180 185 190	
tgg gct ctt ggt gtg atc aca tat gct tta ctt agc gga ttc ctg cct	624
Trp Ala Leu Gly Val Ile Thr Tyr Ala Leu Leu Ser Gly Phe Leu Pro	
195 200 205	
ttt gat gat gaa agc cag aca agg ctt tac agg aag att ctg aaa ggc	672
Phe Asp Asp Glu Ser Gln Thr Arg Leu Tyr Arg Lys Ile Leu Lys Gly	
210 215 220	
aaa tat aat tat aca gga gag cct tgg cca agc att tcc cac ttg gcg	720
Lys Tyr Asn Tyr Thr Gly Glu Pro Trp Pro Ser Ile Ser His Leu Ala	
225 230 235 240	
aag gac ttt ata gac aaa cta ctg att ttg gag gct ggt cat cgc atg	768
Lys Asp Phe Ile Asp Lys Leu Leu Ile Leu Glu Ala Gly His Arg Met	
245 250 255	
tca gct ggc cag gcc ctg gac cat ccc tgg gtg atc acc atg gct gca	816
Ser Ala Gly Gln Ala Leu Asp His Pro Trp Val Ile Thr Met Ala Ala	
260 265 270	
ggg tct tcc atg aag aat ctc cag agg gcc ata tcc cga aac ctc atg	864
Gly Ser Ser Met Lys Asn Leu Gln Arg Ala Ile Ser Arg Asn Leu Met	
275 280 285	
cag agg gcc tct ccc cac tct cag agt cct gga tct gca cag tct tct	912
Gln Arg Ala Ser Pro His Ser Gln Ser Pro Gly Ser Ala Gln Ser Ser	
290 295 300	
aag tca cat tat tct cac aaa tcc agg cat ata gtc aaa agc aaa gga	960
Lys Ser His Tyr Ser His Lys Ser Arg His Ile Val Lys Ser Lys Gly	
305 310 315 320	
aag gcc aac aaa agc cac aga ata tct ttg tta ttc cta gca gat ttt	1008
Lys Ala Asn Lys Ser His Arg Ile Ser Leu Leu Phe Leu Ala Asp Phe	
325 330 335	

39/155

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ttt cac aag aag att aag aat ata att gtt gtt tat atc cca gcc tat 1056
Phe His Lys Lys Ile Lys Asn Ile Ile Val Val Tyr Ile Pro Ala Tyr
          340                      345          350

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aat tta tca gaa gag aaa aac ggg aaa atg gaa tct 1092
Asn Leu Ser Glu Glu Lys Asn Gly Lys Met Glu Ser
          355                      360

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<210> 22
<211> 364
<212> PRT
<213> Homo sapiens

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<400> 22
Thr Cys Leu Val Phe Leu Pro Asn Arg Tyr Asp Ile Lys Ala Leu Ile
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Gly Thr Gly Ser Phe Ser Arg Val Val Arg Val Glu Gln Lys Thr Thr
 20      25      30
Lys Lys Pro Phe Ala Ile Lys Val Met Glu Thr Arg Glu Arg Glu Gly
 35      40      45
Arg Glu Ala Cys Val Ser Glu Leu Ser Val Leu Arg Arg Val Ser His
 50      55      60
Arg Tyr Ile Val Gln Leu Met Glu Ile Phe Glu Thr Glu Asp Gln Val
 65      70      75      80
Tyr Met Val Met Glu Leu Ala Thr Gly Gly Glu Leu Phe Asp Arg Leu
 85      90      95
Ile Ala Gln Gly Ser Phe Thr Glu Arg Asp Ala Val Arg Ile Leu Gln
 100     105     110
Met Val Ala Asp Gly Ile Arg Tyr Leu His Ala Leu Gln Ile Thr His
 115     120     125
Arg Asn Leu Lys Pro Glu Asn Leu Leu Tyr Tyr His Pro Gly Glu Glu
 130     135     140
Ser Lys Ile Leu Ile Thr Asp Phe Gly Leu Ala Tyr Ser Gly Lys Lys
 145     150     155     160
Ser Gly Asp Trp Thr Met Lys Thr Leu Cys Gly Thr Pro Glu Tyr Ile
 165     170     175
Ala Pro Glu Val Leu Leu Arg Lys Pro Tyr Thr Ser Ala Val Asp Met
 180     185     190
Trp Ala Leu Gly Val Ile Thr Tyr Ala Leu Leu Ser Gly Phe Leu Pro
 195     200     205
Phe Asp Asp Glu Ser Gln Thr Arg Leu Tyr Arg Lys Ile Leu Lys Gly
 210     215     220
Lys Tyr Asn Tyr Thr Gly Glu Pro Trp Pro Ser Ile Ser His Leu Ala
 225     230     235     240
Lys Asp Phe Ile Asp Lys Leu Leu Ile Leu Glu Ala Gly His Arg Met
 245     250     255
Ser Ala Gly Gln Ala Leu Asp His Pro Trp Val Ile Thr Met Ala Ala
 260     265     270
Gly Ser Ser Met Lys Asn Leu Gln Arg Ala Ile Ser Arg Asn Leu Met
 275     280     285
Gln Arg Ala Ser Pro His Ser Gln Ser Pro Gly Ser Ala Gln Ser Ser
 290     295     300
Lys Ser His Tyr Ser His Lys Ser Arg His Ile Val Lys Ser Lys Gly
 305     310     315     320
Lys Ala Asn Lys Ser His Arg Ile Ser Leu Leu Phe Leu Ala Asp Phe
 325     330     335
Phe His Lys Lys Ile Lys Asn Ile Ile Val Val Tyr Ile Pro Ala Tyr
 340     345     350
Asn Leu Ser Glu Glu Lys Asn Gly Lys Met Glu Ser
 355     360

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40/155

<210> 23
 <211> 1158
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1158)
 <223> MOOSE03309

<400> 23
 cag acc acc aac atc cgg aaa acc ttc att ttt atg gaa gtg ctg gga 48
 Gln Thr Thr Asn Ile Arg Lys Thr Phe Ile Phe Met Glu Val Leu Gly
 1 5 10 15

tca gga gct ttc tca gaa gtt ttc ctg gtg aag caa aga ctg act ggg 96
 Ser Gly Ala Phe Ser Glu Val Phe Leu Val Lys Gln Arg Leu Thr Gly
 20 25 30

aag ctc ttt gct ctg aag tgc atc aag aag tca cct gcc ttc cgg gac 144
 Lys Leu Phe Ala Leu Lys Cys Ile Lys Lys Ser Pro Ala Phe Arg Asp
 35 40 45

agc agc ctg gag aat gag att gct gtg ttg aaa aag atc aag cat gaa 192
 Ser Ser Leu Glu Asn Glu Ile Ala Val Leu Lys Lys Ile Lys His Glu
 50 55 60

aac att gtg acc ctg gag gac atc tat gag agc acc acc cac tac tac 240
 Asn Ile Val Thr Leu Glu Asp Ile Tyr Glu Ser Thr Thr His Tyr Tyr
 65 70 75 80

ctg gtc atg cag ctt gtt tct ggt ggg gag ctc ttt gac cgg atc ctg 288
 Leu Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Leu
 85 90 95

gag cgg ggt gtc tac aca gag aag gat gcc agt ctg gtg atc cag cag 336
 Glu Arg Gly Val Tyr Thr Glu Lys Asp Ala Ser Leu Val Ile Gln Gln
 100 105 110

gtc ttg tcg gca gtg aaa tac cta cat gag aat ggc atc gtc cac aga 384
 Val Leu Ser Ala Val Lys Tyr Leu His Glu Asn Gly Ile Val His Arg
 115 120 125

gac tta aag ccc gaa aac ctg ctt tac ctt acc cct gaa gag aac tct 432
 Asp Leu Lys Pro Glu Asn Leu Leu Tyr Leu Thr Pro Glu Glu Asn Ser
 130 135 140

aag atc atg atc act gac ttt ggt ctg tcc aag atg gaa cag aat ggc 480
 Lys Ile Met Ile Thr Asp Phe Gly Leu Ser Lys Met Glu Gln Asn Gly
 145 150 155 160

atc atg tcc act gcc tgt ggg acc cca ggc tac gtg gct cca gaa gtg 528
 Ile Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val
 165 170 175

ctg gcc cag aaa ccc tac agc aag gct gtg gat tgc tgg tcc atc ggc 576
 Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly
 180 185 190

gtc atc acc tac ata ttg ctc tgt gga tac ccc cca ttc tat gaa gaa 624
 Val Ile Thr Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Glu Glu
 195 200 205

41/155

acg gag tct aag ctt ttc gag aag atc aag gag ggc tac tat gag ttt	672
Thr Glu Ser Lys Leu Phe Glu Lys Ile Lys Glu Gly Tyr Tyr Glu Phe	
210 215 220	
gag tct cca ttc tgg gat gac att tct gag tca gcc aag gac ttt att	720
Glu Ser Pro Phe Trp Asp Asp Ile Ser Glu Ser Ala Lys Asp Phe Ile	
225 230 235 240	
tgc cac ttg ctt gag aag gat ccg aac gag cgg tac acc tgt gag aag	768
Cys His Leu Leu Glu Lys Asp Pro Asn Glu Arg Tyr Thr Cys Glu Lys	
245 250 255	
gcc ttg agt cat ccc tgg gtg caa tgt tca gta cta gtt att caa gaa	816
Ala Leu Ser His Pro Trp Val Gln Cys Ser Val Leu Val Ile Gln Glu	
260 265 270	
aaa cct cta gac cca gct ccc ctg aga tca cca tca ccg agg cac ctg	864
Lys Pro Leu Asp Pro Ala Pro Leu Arg Ser Pro Ser Pro Arg His Leu	
275 280 285	
tcc tgg acc aca gtg gga gag ggg aga cga tcc aga gag agg aaa aac	912
Ser Trp Thr Thr Val Gly Glu Gly Arg Arg Ser Arg Glu Arg Lys Asn	
290 295 300	
att cgc aaa ggc aag agg caa gag aaa gtg tat ggc ggt gtt aaa gag	960
Ile Arg Lys Gly Lys Arg Gln Glu Lys Val Tyr Gly Gly Val Lys Glu	
305 310 315 320	
gct acc caa agc ccc tca ata acc aat ccc acc cca cac ctg gga aac	1008
Ala Thr Gln Ser Pro Ser Ile Thr Asn Pro Thr Pro His Leu Gly Asn	
325 330 335	
caa cag cca gac atc tcc atg aca acc aag cac cag aaa cag cca gac	1056
Gln Gln Pro Asp Ile Ser Met Thr Thr Lys His Gln Lys Gln Pro Asp	
340 345 350	
atc tcc atg aga gct aag gac cag aaa ctg gtt tcc ttg gca acc act	1104
Ile Ser Met Arg Ala Lys Asp Gln Lys Leu Val Ser Leu Ala Thr Thr	
355 360 365	
gag ctc aca gtg agc agt aca agg gtc ggg atg gct ggg gga gtg ggg	1152
Glu Leu Thr Val Ser Ser Thr Arg Val Gly Met Ala Gly Gly Val Gly	
370 375 380	
ttc tca	1158
Phe Ser	
385	
<210> 24	
<211> 386	
<212> PRT	
<213> Homo sapiens	
<400> 24	
Gln Thr Thr Asn Ile Arg Lys Thr Phe Ile Phe Met Glu Val Leu Gly	
1 5 10 15	
Ser Gly Ala Phe Ser Glu Val Phe Leu Val Lys Gln Arg Leu Thr Gly	
20 25 30	
Lys Leu Phe Ala Leu Lys Cys Ile Lys Lys Ser Pro Ala Phe Arg Asp	
35 40 45	

42/155

```

Ser Ser Leu Glu Asn Glu Ile Ala Val Leu Lys Lys Ile Lys His Glu
  50      55      60
Asn Ile Val Thr Leu Glu Asp Ile Tyr Glu Ser Thr Thr His Tyr Tyr
  65      70      75      80
Leu Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Leu
      85      90      95
Glu Arg Gly Val Tyr Thr Glu Lys Asp Ala Ser Leu Val Ile Gln Gln
      100      105      110
Val Leu Ser Ala Val Lys Tyr Leu His Glu Asn Gly Ile Val His Arg
      115      120      125
Asp Leu Lys Pro Glu Asn Leu Leu Tyr Leu Thr Pro Glu Glu Asn Ser
      130      135      140
Lys Ile Met Ile Thr Asp Phe Gly Leu Ser Lys Met Glu Gln Asn Gly
      145      150      155      160
Ile Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val
      165      170      175
Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly
      180      185      190
Val Ile Thr Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Glu Glu
      195      200      205
Thr Glu Ser Lys Leu Phe Glu Lys Ile Lys Glu Gly Tyr Tyr Glu Phe
      210      215      220
Glu Ser Pro Phe Trp Asp Asp Ile Ser Glu Ser Ala Lys Asp Phe Ile
      225      230      235      240
Cys His Leu Leu Glu Lys Asp Pro Asn Glu Arg Tyr Thr Cys Glu Lys
      245      250      255
Ala Leu Ser His Pro Trp Val Gln Cys Ser Val Leu Val Ile Gln Glu
      260      265      270
Lys Pro Leu Asp Pro Ala Pro Leu Arg Ser Pro Ser Pro Arg His Leu
      275      280      285
Ser Trp Thr Thr Val Gly Glu Gly Arg Arg Ser Arg Glu Arg Lys Asn
      290      295      300
Ile Arg Lys Gly Lys Arg Gln Glu Lys Val Tyr Gly Gly Val Lys Glu
      305      310      315      320
Ala Thr Gln Ser Pro Ser Ile Thr Asn Pro Thr Pro His Leu Gly Asn
      325      330      335
Gln Gln Pro Asp Ile Ser Met Thr Thr Lys His Gln Lys Gln Pro Asp
      340      345      350
Ile Ser Met Arg Ala Lys Asp Gln Lys Leu Val Ser Leu Ala Thr Thr
      355      360      365
Glu Leu Thr Val Ser Ser Thr Arg Val Gly Met Ala Gly Gly Val Gly
      370      375      380
Phe Ser
385

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<210> 25
<211> 1260
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)...(1260)
<223> MOOSE03312

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<400> 25
gaa tca tca act ctt ctt gag aaa tac aaa att gga aag gtc att ggt   48
Glu Ser Ser Thr Leu Leu Glu Lys Tyr Lys Ile Gly Lys Val Ile Gly
  1              5              10              15

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43/155

gat ggc aat ttt gca gta gtc aaa gag tgt ata gac agg tcc act gga	96
Asp Gly Asn Phe 20 Ala Val Val Lys 25 Glu Cys Ile Asp Arg 30 Ser Thr Gly	
aag gag ttt gcc cta aag att ata gac aaa gcc aaa tgt tgt gga aag	144
Lys Glu Phe Ala Leu Lys Ile Ile 40 Asp Lys Ala Lys Cys 45 Cys Gly Lys	
gaa cac ctg att gag aat gaa gtg tca ata ctg cgc cga gtg aaa cat	192
Glu His Leu Ile Glu Asn Glu Val Ser Ile Leu Arg Arg Val Lys His	
50 55 60	
ccc aat atc att atg ctg gtc gag gag atg gaa aca gca act gag ctc	240
Pro Asn Ile Ile Met 70 Leu Val Glu Glu Met 75 Glu Thr Ala Thr Glu Leu	
65 80	
ttt ctg gtg atg gaa ttg gtc aaa ggt gga gat ctc ttt gat gca att	288
Phe Leu Val Met 85 Glu Leu Val Lys Gly Gly 90 Asp Leu Phe Asp Ala Ile	
95	
act tcg tcg acc aag tac act gag aga gat ggc agt gcc atg gtg tac	336
Thr Ser Ser Thr Lys Tyr Thr Glu Arg Asp Gly Ser Ala Met Val Tyr	
100 105 110	
aac tta gcc aat gcc ctc agg tat ctc cat ggc ctc agc atc gtg cac	384
Asn Leu Ala Asn Ala Leu Arg Tyr Leu His Gly Leu Ser Ile Val His	
115 120 125	
aga gac atc aaa cca gag aat ctc ttg gtg tgt gaa tat cct gat gga	432
Arg Asp Ile Lys Pro Glu Asn Leu Leu Val Cys Glu Tyr Pro Asp Gly	
130 135 140	
acc aag tct ttg aaa ctg gga gac ttt ggg ctt gcg act gtg gta gaa	480
Thr Lys Ser Leu Lys Leu Gly Asp Phe Gly Leu Ala Thr Val Val Glu	
145 150 155 160	
ggc cct tta tac aca gtc tgt ggc aca ccc act tat gtg gct cca gaa	528
Gly Pro Leu Tyr Thr Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu	
165 170 175	
atc att gct gaa act ggc tat ggc ctg aag gtg gac att tgg gca gct	576
Ile Ile Ala Glu Thr Gly Tyr Gly Leu Lys Val Asp Ile Trp Ala Ala	
180 185 190	
ggg gtg atc aca tac ata ctt ctc tgt gga ttc cca cca ttc cga agt	624
Gly Val Ile Thr Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser	
195 200 205	
gag aac aat ctc cag gaa gat ctc ttc gac cag atc ttg gct ggg aag	672
Glu Asn Asn Leu Gln Glu Asp Leu Phe Asp Gln Ile Leu Ala Gly Lys	
210 215 220	
ctg gag ttt ccg gcc ccc tac tgg gat aac atc acg gac tct gcc aag	720
Leu Glu Phe Pro Ala Pro Tyr Trp Asp Asn Ile Thr Asp Ser Ala Lys	
225 230 235 240	
gaa tta atc agt caa atg ctt cag gta aat gtt gaa gct cgg tgt acc	768
Glu Leu Ile Ser Gln Met Leu Gln Val Asn Val Glu Ala Arg Cys Thr	
245 250 255	

44 / 155

[illegible]

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<210> 26
<211> 420
<212> PRT
<213> Homo sapiens
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<400> 26															
Glu	Ser	Ser	Thr	Leu	Leu	Glu	Lys	Tyr	Lys	Ile	Gly	Lys	Val	Ile	Gly
1				5					10					15	
Asp	Gly	Asn	Phe	Ala	Val	Val	Lys	Glu	Cys	Ile	Asp	Arg	Ser	Thr	Gly
			20					25					30		
Lys	Glu	Phe	Ala	Leu	Lys	Ile	Ile	Asp	Lys	Ala	Lys	Cys	Cys	Gly	Lys
		35				40						45			
Glu	His	Leu	Ile	Glu	Asn	Glu	Val	Ser	Ile	Leu	Arg	Arg	Val	Lys	His
	50					55					60				
Pro	Asn	Ile	Ile	Met	Leu	Val	Glu	Glu	Met	Glu	Thr	Ala	Thr	Glu	Leu
65					70					75					80

45/155

Phe Leu Val Met Glu Leu Val Lys Gly Gly Asp Leu Phe Asp Ala Ile
 85 90 95
 Thr Ser Ser Thr Lys Tyr Thr Glu Arg Asp Gly Ser Ala Met Val Tyr
 100 105 110
 Asn Leu Ala Asn Ala Leu Arg Tyr Leu His Gly Leu Ser Ile Val His
 115 120 125
 Arg Asp Ile Lys Pro Glu Asn Leu Leu Val Cys Glu Tyr Pro Asp Gly
 130 135 140
 Thr Lys Ser Leu Lys Leu Gly Asp Phe Gly Leu Ala Thr Val Val Glu
 145 150 155 160
 Gly Pro Leu Tyr Thr Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu
 165 170 175
 Ile Ile Ala Glu Thr Gly Tyr Gly Leu Lys Val Asp Ile Trp Ala Ala
 180 185 190
 Gly Val Ile Thr Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser
 195 200 205
 Glu Asn Asn Leu Gln Glu Asp Leu Phe Asp Gln Ile Leu Ala Gly Lys
 210 215 220
 Leu Glu Phe Pro Ala Pro Tyr Trp Asp Asn Ile Thr Asp Ser Ala Lys
 225 230 235 240
 Glu Leu Ile Ser Gln Met Leu Gln Val Asn Val Glu Ala Arg Cys Thr
 245 250 255
 Ala Gly Gln Ile Leu Ser His Pro Trp Val Ser Pro Met Gln Pro Trp
 260 265 270
 Ala Gly Arg Pro Ala His Arg Glu Gln Val Glu Ala Ser Gln Pro Pro
 275 280 285
 Arg Gln Gly Pro Trp Phe Ser Pro His Thr Pro Arg Ser Arg Glu Gln
 290 295 300
 Gly Trp Ser Gly Leu Ser Gln Ser Trp Ser Trp Leu Gln Gln Leu Ser
 305 310 315 320
 Asn Gln Thr Cys Gln Gly Asp Gly Arg Leu Ser Phe Thr Ser Gly Pro
 325 330 335
 Pro Thr Leu Ser Leu Gln Lys Lys Lys Ile Phe Phe Ser Lys Phe Met
 340 345 350
 Ala Ala Thr Asn His Val Ala Val Gln His Trp Lys Cys Ala Leu Ser
 355 360 365
 Lys Leu Arg His Ala Ile Asn Val Lys His Thr Arg Phe Gln Ser His
 370 375 380
 Glu Asp Ile Leu Gly Glu Val Leu Pro Asn Ala Phe Asn Leu Tyr Ile
 385 390 395 400
 Gln Tyr Ile Ser Ile Ile Ala Thr Phe Leu Lys Arg Glu Gly Glu Arg
 405 410 415
 Lys Arg Glu Lys
 420

<210> 27
 <211> 1299
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1299)
 <223> MOOSE03313

<400> 27
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 Asp Ala Ala Val Leu Lys Arg Arg Gly Tyr Leu Leu Gly Ile Asn Leu
 1 5 10 15

46/155

gga gag ggc tcc tat gca aaa gta aaa tct gct tac tct gag cgc ctg	96
Gly Glu Gly Ser Tyr Ala Lys Val Lys Ser Ala Tyr Ser Glu Arg Leu	
20 25 30	
aag ttc aat gtg gcg atc aag atc atc gac cgc aag aag gcc ccc gca	144
Lys Phe Asn Val Ala Ile Lys Ile Ile Asp Arg Lys Lys Ala Pro Ala	
35 40 45	
gac ttc ttg gag aaa ttc ctt ccc cgg gaa att gag att ctg gcc atg	192
Asp Phe Leu Glu Lys Phe Leu Pro Arg Glu Ile Glu Ile Leu Ala Met	
50 55 60	
tta aac cac tgc tcc atc att aag acc tac gag atc ttt gag aca tca	240
Leu Asn His Cys Ser Ile Ile Lys Thr Tyr Glu Ile Phe Glu Thr Ser	
65 70 75 80	
cat ggc aag gtc tac atc gtc atg gag ctc gca gtc cag gcc gac ctc	288
His Gly Lys Val Tyr Ile Val Met Glu Leu Ala Val Gln Gly Asp Leu	
85 90 95	
ctc gag tta atc aaa acc cgg gga gcc ctg cat gag gac gaa gct cgc	336
Leu Glu Leu Ile Lys Thr Arg Gly Ala Leu His Glu Asp Glu Ala Arg	
100 105 110	
aag aag ttc cac cag ctt tcc ttg gcc atc aag tac tgc cac gac ctg	384
Lys Lys Phe His Gln Leu Ser Leu Ala Ile Lys Tyr Cys His Asp Leu	
115 120 125	
gac gtc gtc cac cgg gac ctc aag tgt gac aac ctt ctc ctt gac aag	432
Asp Val Val His Arg Asp Leu Lys Cys Asp Asn Leu Leu Leu Asp Lys	
130 135 140	
gac ttc aac atc aag ctg tcc gac ttc agc ttc tcc aag cgc tgc ctg	480
Asp Phe Asn Ile Lys Leu Ser Asp Phe Ser Phe Ser Lys Arg Cys Leu	
145 150 155 160	
cgg gat gac agt ggt cga atg gcc tta agc aag acc ttc tgt ggg tca	528
Arg Asp Asp Ser Gly Arg Met Ala Leu Ser Lys Thr Phe Cys Gly Ser	
165 170 175	
cca gcg tat gcg gcc cca gag gtg ctg cag ggc att ccc tac cag ccc	576
Pro Ala Tyr Ala Ala Pro Glu Val Leu Gln Gly Ile Pro Tyr Gln Pro	
180 185 190	
aag gtg tac gac atc tgg agc cta ggc gtg atc ctc tac atc atg gtc	624
Lys Val Tyr Asp Ile Trp Ser Leu Gly Val Ile Leu Tyr Ile Met Val	
195 200 205	
tgc ggc tcc atg ccc tac gac gac tcc aac atc aag aag atg ctg cgt	672
Cys Gly Ser Met Pro Tyr Asp Asp Ser Asn Ile Lys Lys Met Leu Arg	
210 215 220	
atc cag aag gag cac cgc gtc aac ttc cca cgc tcc aag cac ctg aca	720
Ile Gln Lys Glu His Arg Val Asn Phe Pro Arg Ser Lys His Leu Thr	
225 230 235 240	
ggc gag tgc aag gac ctc atc tac cac atg ctg cag ccc gac gtc aac	768
Gly Glu Cys Lys Asp Leu Ile Tyr His Met Leu Gln Pro Asp Val Asn	
245 250 255	

47/155

cgg cgg ctc cac atc gac gag atc ctc agc cac tgc tgg atg cag ccc 816
 Arg Arg Leu His Ile Asp Glu Ile Leu Ser His Cys Trp Met Gln Pro
 260 265 270

aag gca cgg gga tct ccc tct gtg gcc atc aac aag gag ggg gag aat 864
 Lys Ala Arg Gly Ser Pro Ser Val Ala Ile Asn Lys Glu Gly Glu Asn
 275 280 285

aaa acc aca aag atg ggg aga aac cag agc aga aaa gct gaa aat tct 912
 Lys Thr Thr Lys Met Gly Arg Asn Gln Ser Arg Lys Ala Glu Asn Ser
 290 295 300

aaa aac cag agt gcc ttt tct cct cca aag gat cac agc tcc tcg cca 960
 Lys Asn Gln Ser Ala Phe Ser Pro Pro Lys Asp His Ser Ser Ser Pro
 305 310 315 320

gca atg gaa caa agc tgg acg gag aat gac ttt gac aag ctg aca gaa 1008
 Ala Met Glu Gln Ser Trp Thr Glu Asn Asp Phe Asp Lys Leu Thr Glu
 325 330 335

gta ggc ttc aga agg tcg gta ata aca aac ttc tcc aag cta aag gag 1056
 Val Gly Phe Arg Arg Ser Val Ile Thr Asn Phe Ser Lys Leu Lys Glu
 340 345 350

gat gtt cga acc cat cac aag gaa gct aaa agc ctt gaa aaa aga tta 1104
 Asp Val Arg Thr His His Lys Glu Ala Lys Ser Leu Glu Lys Arg Leu
 355 360 365

gac caa tgg cta aat aga ata aac agt gta gag gag acc tta aat gac 1152
 Asp Gln Trp Leu Asn Arg Ile Asn Ser Val Glu Glu Thr Leu Asn Asp
 370 375 380

ctg atg gag ctg aaa acc atg gca cga gaa cta cgt gac gca tgc aca 1200
 Leu Met Glu Leu Lys Thr Met Ala Arg Glu Leu Arg Asp Ala Cys Thr
 385 390 395 400

aga ttt aat agc caa ttc gat caa gtg gaa gaa agg gta tca gtg att 1248
 Arg Phe Asn Ser Gln Phe Asp Gln Val Glu Glu Arg Val Ser Val Ile
 405 410 415

gaa gat caa att aat gaa ata aag caa gaa gag aaa gtt aga gaa aaa 1296
 Glu Asp Gln Ile Asn Glu Ile Lys Gln Glu Glu Lys Val Arg Glu Lys
 420 425 430

agc 1299
 Ser

<210> 28
 <211> 433
 <212> PRT
 <213> Homo sapiens

<400> 28
 Asp Ala Ala Val Leu Lys Arg Arg Gly Tyr Leu Leu Gly Ile Asn Leu
 1 5 10 15
 Gly Glu Gly Ser Tyr Ala Lys Val Lys Ser Ala Tyr Ser Glu Arg Leu
 20 25 30
 Lys Phe Asn Val Ala Ile Lys Ile Ile Asp Arg Lys Lys Ala Pro Ala
 35 40 45

48/155

```

Asp Phe Leu Glu Lys Phe Leu Pro Arg Glu Ile Glu Ile Leu Ala Met
 50      55      60
Leu Asn His Cys Ser Ile Ile Lys Thr Tyr Glu Ile Phe Glu Thr Ser
 65      70      75      80
His Gly Lys Val Tyr Ile Val Met Glu Leu Ala Val Gln Gly Asp Leu
      85      90      95
Leu Glu Leu Ile Lys Thr Arg Gly Ala Leu His Glu Asp Glu Ala Arg
      100      105      110
Lys Lys Phe His Gln Leu Ser Leu Ala Ile Lys Tyr Cys His Asp Leu
      115      120      125
Asp Val Val His Arg Asp Leu Lys Cys Asp Asn Leu Leu Leu Asp Lys
      130      135      140
Asp Phe Asn Ile Lys Leu Ser Asp Phe Ser Phe Ser Lys Arg Cys Leu
      145      150      155      160
Arg Asp Asp Ser Gly Arg Met Ala Leu Ser Lys Thr Phe Cys Gly Ser
      165      170      175
Pro Ala Tyr Ala Ala Pro Glu Val Leu Gln Gly Ile Pro Tyr Gln Pro
      180      185      190
Lys Val Tyr Asp Ile Trp Ser Leu Gly Val Ile Leu Tyr Ile Met Val
      195      200      205
Cys Gly Ser Met Pro Tyr Asp Asp Ser Asn Ile Lys Lys Met Leu Arg
      210      215      220
Ile Gln Lys Glu His Arg Val Asn Phe Pro Arg Ser Lys His Leu Thr
      225      230      235      240
Gly Glu Cys Lys Asp Leu Ile Tyr His Met Leu Gln Pro Asp Val Asn
      245      250      255
Arg Arg Leu His Ile Asp Glu Ile Leu Ser His Cys Trp Met Gln Pro
      260      265      270
Lys Ala Arg Gly Ser Pro Ser Val Ala Ile Asn Lys Glu Gly Glu Asn
      275      280      285
Lys Thr Thr Lys Met Gly Arg Asn Gln Ser Arg Lys Ala Glu Asn Ser
      290      295      300
Lys Asn Gln Ser Ala Phe Ser Pro Pro Lys Asp His Ser Ser Ser Pro
      305      310      315      320
Ala Met Glu Gln Ser Trp Thr Glu Asn Asp Phe Asp Lys Leu Thr Glu
      325      330      335
Val Gly Phe Arg Arg Ser Val Ile Thr Asn Phe Ser Lys Leu Lys Glu
      340      345      350
Asp Val Arg Thr His His Lys Glu Ala Lys Ser Leu Glu Lys Arg Leu
      355      360      365
Asp Gln Trp Leu Asn Arg Ile Asn Ser Val Glu Glu Thr Leu Asn Asp
      370      375      380
Leu Met Glu Leu Lys Thr Met Ala Arg Glu Leu Arg Asp Ala Cys Thr
      385      390      395      400
Arg Phe Asn Ser Gln Phe Asp Gln Val Glu Glu Arg Val Ser Val Ile
      405      410      415
Glu Asp Gln Ile Asn Glu Ile Lys Gln Glu Glu Lys Val Arg Glu Lys
      420      425      430
Ser

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<210> 29
 <211> 1215
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1215)
 <223> MOOSE03314

49/155

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gac gct gct gtc ctc aag cga cga ggc tac ctc ctg ggg ata aat tta 48
Asp Ala Ala Val Leu Lys Arg Arg Gly Tyr Leu Leu Gly Ile Asn Leu
1 5 10 15

gga gag ggc tcc tat gca aaa gta aaa tct gct tac tct gag cgc ctg 96
Gly Glu Gly Ser Tyr Ala Lys Val Lys Ser Ala Tyr Ser Glu Arg Leu
20 25 30

aag ttc aat gtg gcg atc aag atc atc gac cgc aag aag gcc ccc gca 144
Lys Phe Asn Val Ala Ile Lys Ile Ile Asp Arg Lys Lys Ala Pro Ala
35 40 45

gac ttc ttg gag aaa ttc ctt ccc cgg gaa att gag att ctg gcc atg 192
Asp Phe Leu Glu Lys Phe Leu Pro Arg Glu Ile Glu Ile Leu Ala Met
50 55 60

tta aac cac tgc tcc atc att aag acc tac gag atc ttt gag aca tca 240
Leu Asn His Cys Ser Ile Ile Lys Thr Tyr Glu Ile Phe Glu Thr Ser
65 70 75 80

cat ggc aag gtc tac atc gtc atg gag ctc gcg gtc cag ggc gac ctc 288
His Gly Lys Val Tyr Ile Val Met Glu Leu Ala Val Gln Gly Asp Leu
85 90 95

ctc gag tta atc aaa acc cgg gga gcc ctg cat gag gac gaa gct cgc 336
Leu Glu Leu Ile Lys Thr Arg Gly Ala Leu His Glu Asp Glu Ala Arg
100 105 110

aag aag ttc cac cag ctt tcc ttg gcc atc aag tac tgc cac gac ctg 384
Lys Lys Phe His Gln Leu Ser Leu Ala Ile Lys Tyr Cys His Asp Leu
115 120 125

gac gtc gtc cac cgg gac ctc aag tgt gac aac ctt ctc ctt gac aag 432
Asp Val Val His Arg Asp Leu Lys Cys Asp Asn Leu Leu Leu Asp Lys
130 135 140

gac ttc aac atc aag ctg tcc gac ttc agc ttc tcc aag cgc tgc ctg 480
Asp Phe Asn Ile Lys Leu Ser Asp Phe Ser Phe Ser Lys Arg Cys Leu
145 150 155 160

cgg gat gac agt ggt cga atg gcc tta agc aag acc ttc tgt ggg tca 528
Arg Asp Asp Ser Gly Arg Met Ala Leu Ser Lys Thr Phe Cys Gly Ser
165 170 175

cca gcg tat gcg gcc cca gag gtg ctg cag ggc att ccc tac cag ccc 576
Pro Ala Tyr Ala Ala Pro Glu Val Leu Gln Gly Ile Pro Tyr Gln Pro
180 185 190

aag gtg tac gac atc tgg agc cta ggc gtg atc ctc tac atc atg gtc 624
Lys Val Tyr Asp Ile Trp Ser Leu Gly Val Ile Leu Tyr Ile Met Val
195 200 205

tgc ggc tcc atg ccc tac gac gac tcc aac atc aag aag atg ctg cgt 672
Cys Gly Ser Met Pro Tyr Asp Asp Ser Asn Ile Lys Lys Met Leu Arg
210 215 220

atc cag aag gag cac cgc gtc aac ttc cca cgc tcc aag cac ctg aca 720
Ile Gln Lys Glu His Arg Val Asn Phe Pro Arg Ser Lys His Leu Thr
225 230 235 240

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50/155

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ggc gag tgc aag gac ctc atc tac cac atg ctg cag ccc gac gtc aac 768
Gly Glu Cys Lys Asp Leu Ile Tyr His Met Leu Gln Pro Asp Val Asn
245 250 255

cgg cgg ctc cac atc gac gag atc ctc agc cac tgc tgg atg cag ccc 816
Arg Arg Leu His Ile Asp Glu Ile Leu Ser His Cys Trp Met Gln Pro
260 265 270

aag gca cgg gga tct ccc tct gtg gcc atc aac aag gag ggg gag agt 864
Lys Ala Arg Gly Ser Pro Ser Val Ala Ile Asn Lys Glu Gly Glu Ser
275 280 285

tcc cgg gga act gaa ccc tta aca gaa gtc ata aca aac agt ctc tca 912
Ser Arg Gly Thr Glu Pro Leu Thr Glu Val Ile Thr Asn Ser Leu Ser
290 295 300

gac cac agt gga atc aaa tta aaa ctc acg att aag aaa ctc act caa 960
Asp His Ser Gly Ile Lys Leu Lys Leu Thr Ile Lys Lys Leu Thr Gln
305 310 315 320

aac tgc aca acc tca tgg aac ctg aac aac aac gtg ctc ctg aat gac 1008
Asn Cys Thr Thr Ser Trp Asn Leu Asn Asn Asn Val Leu Leu Asn Asp
325 330 335

tac tgg gta aat aac gaa att aag gca gaa ata att aag ttc ttt gaa 1056
Tyr Trp Val Asn Asn Glu Ile Lys Ala Glu Ile Ile Lys Phe Phe Glu
340 345 350

acc aat gag aac aaa gac aca tca tac cag aat ctc tgg aca cta gct 1104
Thr Asn Glu Asn Lys Asp Thr Ser Tyr Gln Asn Leu Trp Thr Leu Ala
355 360 365

aaa gca gtg ttt aga ggg aaa ttt ata gaa cta aat gcc cac aag aga 1152
Lys Ala Val Phe Arg Gly Lys Phe Ile Glu Leu Asn Ala His Lys Arg
370 375 380

aag cag gaa agg tct aaa att gac acc cta aca tca caa tta aag gaa 1200
Lys Gln Glu Arg Ser Lys Ile Asp Thr Leu Thr Ser Gln Leu Lys Glu
385 390 395 400

cta gaa agc aga gca
Leu Glu Ser Arg Ala
405

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<210> 30

<211> 405

<212> PRT

<213> Homo sapiens

<400> 30

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Asp Ala Ala Val Leu Lys Arg Arg Gly Tyr Leu Leu Gly Ile Asn Leu
1 5 10 15
Gly Glu Gly Ser Tyr Ala Lys Val Lys Ser Ala Tyr Ser Glu Arg Leu
20 25 30
Lys Phe Asn Val Ala Ile Lys Ile Ile Asp Arg Lys Lys Ala Pro Ala
35 40 45
Asp Phe Leu Glu Lys Phe Leu Pro Arg Glu Ile Glu Ile Leu Ala Met
50 55 60
Leu Asn His Cys Ser Ile Ile Lys Thr Tyr Glu Ile Phe Glu Thr Ser
65 70 75 80

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51/155

His Gly Lys Val Tyr Ile Val Met Glu Leu Ala Val Gln Gly Asp Leu
 85 90 95
 Leu Glu Leu Ile Lys Thr Arg Gly Ala Leu His Glu Asp Glu Ala Arg
 100 105 110
 Lys Lys Phe His Gln Leu Ser Leu Ala Ile Lys Tyr Cys His Asp Leu
 115 120 125
 Asp Val Val His Arg Asp Leu Lys Cys Asp Asn Leu Leu Asp Lys
 130 135 140
 Asp Phe Asn Ile Lys Leu Ser Asp Phe Ser Phe Ser Lys Arg Cys Leu
 145 150 155 160
 Arg Asp Asp Ser Gly Arg Met Ala Leu Ser Lys Thr Phe Cys Gly Ser
 165 170 175
 Pro Ala Tyr Ala Ala Pro Glu Val Leu Gln Gly Ile Pro Tyr Gln Pro
 180 185 190
 Lys Val Tyr Asp Ile Trp Ser Leu Gly Val Ile Leu Tyr Ile Met Val
 195 200 205
 Cys Gly Ser Met Pro Tyr Asp Asp Ser Asn Ile Lys Lys Met Leu Arg
 210 215 220
 Ile Gln Lys Glu His Arg Val Asn Phe Pro Arg Ser Lys His Leu Thr
 225 230 235 240
 Gly Glu Cys Lys Asp Leu Ile Tyr His Met Leu Gln Pro Asp Val Asn
 245 250 255
 Arg Arg Leu His Ile Asp Glu Ile Leu Ser His Cys Trp Met Gln Pro
 260 265 270
 Lys Ala Arg Gly Ser Pro Ser Val Ala Ile Asn Lys Glu Gly Glu Ser
 275 280 285
 Ser Arg Gly Thr Glu Pro Leu Thr Glu Val Ile Thr Asn Ser Leu Ser
 290 295 300
 Asp His Ser Gly Ile Lys Leu Lys Leu Thr Ile Lys Lys Leu Thr Gln
 305 310 315 320
 Asn Cys Thr Thr Ser Trp Asn Leu Asn Asn Val Leu Leu Asn Asp
 325 330 335
 Tyr Trp Val Asn Asn Glu Ile Lys Ala Glu Ile Ile Lys Phe Phe Glu
 340 345 350
 Thr Asn Glu Asn Lys Asp Thr Ser Tyr Gln Asn Leu Trp Thr Leu Ala
 355 360 365
 Lys Ala Val Phe Arg Gly Lys Phe Ile Glu Leu Asn Ala His Lys Arg
 370 375 380
 Lys Gln Glu Arg Ser Lys Ile Asp Thr Leu Thr Ser Gln Leu Lys Glu
 385 390 395 400
 Leu Glu Ser Arg Ala
 405

<210> 31
 <211> 1095
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(1095)
 <223> MOOSE03316

<400> 31
 gat gcc aca gtc cta agg aag aag ggt tac atc gta ggc atc aat ctt 48
 Asp Ala Thr Val Leu Arg Lys Lys Gly Tyr Ile Val Gly Ile Asn Leu
 1 5 10 15
 ggc aag ggt tcc tac gca aaa gtc aaa tct gcc tac tct gag cgc ctc 96
 Gly Lys Gly Ser Tyr Ala Lys Val Lys Ser Ala Tyr Ser Glu Arg Leu
 20 25 30

52/155

aag ttc aat gtg gct gtc aag atc atc gac cgc aag aaa aca cct act	144
Lys Phe Asn Val Ala Val Lys Ile Ile Asp Arg Lys Lys Thr Pro Thr	
35 40 45	
gac ttt gtg gag aga ttc ctt cct cgg gag atg gac atc ctg gca act	192
Asp Phe Val Glu Arg Phe Leu Pro Arg Glu Met Asp Ile Leu Ala Thr	
50 55 60	
gtc aac cac ggc tcc atc atc aag act tac gag atc ttt gag acc tct	240
Val Asn His Gly Ser Ile Ile Lys Thr Tyr Glu Ile Phe Glu Thr Ser	
65 70 75 80	
gac gga cgg atc tac atc atc atg gag ctt ggc gtc cag ggc gac ctc	288
Asp Gly Arg Ile Tyr Ile Ile Met Glu Leu Gly Val Gln Gly Asp Leu	
85 90 95	
ctc gag ttc atc aag tgc cag gga gcc ctg cat gag gac gtg gca cgc	336
Leu Glu Phe Ile Lys Cys Gln Gly Ala Leu His Glu Asp Val Ala Arg	
100 105 110	
aag atg ttc cga cag ctc tcc tcc gcc gtc aag tac tgc cac gac ctg	384
Lys Met Phe Arg Gln Leu Ser Ser Ala Val Lys Tyr Cys His Asp Leu	
115 120 125	
gac atc gtc cac cgg gac ctc aag tgc gag aac ctt ctc ctc gac aag	432
Asp Ile Val His Arg Asp Leu Lys Cys Glu Asn Leu Leu Leu Asp Lys	
130 135 140	
gac ttc aac atc aag ctg tct gac ttt ggc ttc tcc aag cgc tgc ctg	480
Asp Phe Asn Ile Lys Leu Ser Asp Phe Gly Phe Ser Lys Arg Cys Leu	
145 150 155 160	
cgg gac agc aat ggg cgc atc atc ctc agc aag acc ttc tgc ggg tcg	528
Arg Asp Ser Asn Gly Arg Ile Ile Leu Ser Lys Thr Phe Cys Gly Ser	
165 170 175	
gca gca tat gca gcc ccc gag gtg ctg cag agc atc ccc tac cag ccc	576
Ala Ala Tyr Ala Ala Pro Glu Val Leu Gln Ser Ile Pro Tyr Gln Pro	
180 185 190	
aag gtg tat gac atc tgg agc ctg ggc gtg atc ctg tac atc atg gtc	624
Lys Val Tyr Asp Ile Trp Ser Leu Gly Val Ile Leu Tyr Ile Met Val	
195 200 205	
tgc ggc tcc atg ccc tat gac gac tcc gac atc agg aag atg ctg cgt	672
Cys Gly Ser Met Pro Tyr Asp Asp Ser Asp Ile Arg Lys Met Leu Arg	
210 215 220	
atc cag aag gag cac cgt gtg gac ttc ccg cgc tcc aag aac ctg acc	720
Ile Gln Lys Glu His Arg Val Asp Phe Pro Arg Ser Lys Asn Leu Thr	
225 230 235 240	
tgc gag tgc aag gac ctc atc tac cgc atg ctg cag ccc gac gtc agc	768
Cys Glu Cys Lys Asp Leu Ile Tyr Arg Met Leu Gln Pro Asp Val Ser	
245 250 255	
cag cgg ctc cac atc gat gag atc ctc agc cac tcg tgg ctg cag ccc	816
Gln Arg Leu His Ile Asp Glu Ile Leu Ser His Ser Trp Leu Gln Pro	
260 265 270	

53/155

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ccc aag ccc aaa gcc acg tct tct gcc tcc ttc aag agg gag ggg gag 864
Pro Lys Pro Lys Ala Thr Ser Ser Ala Ser Phe Lys Arg Glu Gly Glu
      275      280      285

ggc aag tac cgc gct gag tgc aaa ctg gac acc aag aca ggc ttg agg 912
Gly Lys Tyr Arg Ala Glu Cys Lys Leu Asp Thr Lys Thr Gly Leu Arg
      290      295      300

ccc gac cac cgg ccc gac cac aag ctt gga gcc aaa acc cag cac cgg 960
Pro Asp His Arg Pro Asp His Lys Leu Gly Ala Lys Thr Gln His Arg
305      310      315      320

ctg ctg gtg ggg aac cta agg gta caa ctt cca agg gct ccg ttt ctc 1008
Leu Leu Val Gly Asn Leu Arg Val Gln Leu Pro Arg Ala Pro Phe Leu
      325      330      335

ctt cat atc ccc cca gag aag cag aaa gca ctg cag gat gtg agc tca 1056
Leu His Ile Pro Pro Glu Lys Gln Lys Ala Leu Gln Asp Val Ser Ser
      340      345      350

act cag aac aca ggt tcc gag tgc cgc aga aag caa cgc 1095
Thr Gln Asn Thr Gly Ser Glu Cys Arg Arg Lys Gln Arg
      355      360      365

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<210> 32

<211> 365

<212> PRT

<213> Homo sapiens

<400> 32

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Asp Ala Thr Val Leu Arg Lys Lys Gly Tyr Ile Val Gly Ile Asn Leu
 1      5      10      15
Gly Lys Gly Ser Tyr Ala Lys Val Lys Ser Ala Tyr Ser Glu Arg Leu
      20      25      30
Lys Phe Asn Val Ala Val Lys Ile Asp Arg Lys Lys Thr Pro Thr
      35      40      45
Asp Phe Val Glu Arg Phe Leu Pro Arg Glu Met Asp Ile Leu Ala Thr
      50      55      60
Val Asn His Gly Ser Ile Ile Lys Thr Tyr Glu Ile Phe Glu Thr Ser
      65      70      75      80
Asp Gly Arg Ile Tyr Ile Ile Met Glu Leu Gly Val Gln Gly Asp Leu
      85      90      95
Leu Glu Phe Ile Lys Cys Gln Gly Ala Leu His Glu Asp Val Ala Arg
      100      105      110
Lys Met Phe Arg Gln Leu Ser Ser Ala Val Lys Tyr Cys His Asp Leu
      115      120      125
Asp Ile Val His Arg Asp Leu Lys Cys Glu Asn Leu Leu Asp Lys
      130      135      140
Asp Phe Asn Ile Lys Leu Ser Asp Phe Gly Phe Ser Lys Arg Cys Leu
      145      150      155      160
Arg Asp Ser Asn Gly Arg Ile Ile Leu Ser Lys Thr Phe Cys Gly Ser
      165      170      175
Ala Ala Tyr Ala Ala Pro Glu Val Leu Gln Ser Ile Pro Tyr Gln Pro
      180      185      190
Lys Val Tyr Asp Ile Trp Ser Leu Gly Val Ile Leu Tyr Ile Met Val
      195      200      205
Cys Gly Ser Met Pro Tyr Asp Asp Ser Asp Ile Arg Lys Met Leu Arg
      210      215      220
Ile Gln Lys Glu His Arg Val Asp Phe Pro Arg Ser Lys Asn Leu Thr
      225      230      235      240

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54 / 155

Cys	Glu	Cys	Lys	Asp 245	Leu	Ile	Tyr	Arg	Met 250	Leu	Gln	Pro	Asp	Val 255	Ser
Gln	Arg	Leu	His 260	Ile	Asp	Glu	Ile	Leu	Ser 265	His	Ser	Trp	Leu	Gln 270	Pro
Pro	Lys	Pro 275	Lys	Ala	Thr	Ser	Ser 280	Ala	Ser	Phe	Lys	Arg 285	Glu	Gly	Glu
Gly	Lys	Tyr	Arg	Ala	Glu	Cys 295	Lys	Leu	Asp	Thr	Lys 300	Thr	Gly	Leu	Arg
Pro 305	Asp	His	Arg	Pro	Asp 310	His	Lys	Leu	Gly	Ala 315	Lys	Thr	Gln	His 320	Arg
Leu	Leu	Val	Gly	Asn 325	Leu	Arg	Val	Gln	Leu 330	Pro	Arg	Ala	Pro	Phe 335	Leu
Leu	His	Ile	Pro 340	Pro	Glu	Lys	Gln	Lys 345	Ala	Leu	Gln	Asp	Val 350	Ser	Ser
Thr	Gln	Asn 355	Thr	Gly	Ser	Glu	Cys 360	Arg	Arg	Lys	Gln	Arg 365			

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<210> 33
<211> 1260
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (1) ... (1260)
<223> MOOSE03330
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<400> 33																	48
agc	atg	gag	gac	ttt	ctg	ctc	tcc	aat	ggg	tac	cag	ctg	ggc	aag	acc		
Ser	Met	Glu	Asp	Phe	Leu	Leu	Ser	Asn	Gly	Tyr	Gln	Leu	Gly	Lys	Thr		
1				5				10				15					
																	96
att	ggg	gaa	ggg	acc	tac	tca	aaa	gtc	aaa	gaa	gca	ttt	tcc	aaa	aaa		
Ile	Gly	Glu	Gly	Thr	Tyr	Ser	Lys	Val	Lys	Glu	Ala	Phe	Ser	Lys	Lys		
		20						25				30					
																	144
cac	caa	aga	aaa	gtg	gca	att	aaa	gtt	ata	gac	aag	atg	gga	ggg	cca		
His	Gln	Arg	Lys	Val	Ala	Ile	Lys	Val	Ile	Asp	Lys	Met	Gly	Gly	Pro		
		35				40						45					
																	192
gaa	gag	ttt	atc	cag	aga	ttc	ctc	cct	cgg	gag	ctc	caa	atc	gtc	cgt		
Glu	Glu	Phe	Ile	Gln	Arg	Phe	Leu	Pro	Arg	Glu	Leu	Gln	Ile	Val	Arg		
50						55				60							
																	240
acc	ctg	gac	cac	aag	aac	atc	atc	cag	gtg	tat	gag	atg	ctg	gag	tct		
Thr	Leu	Asp	His	Lys	Asn	Ile	Ile	Gln	Val	Tyr	Glu	Met	Leu	Glu	Ser		
65				70						75				80			
																	288
gcc	gac	ggg	aaa	atc	tgc	ctg	gtg	atg	gag	ctc	gct	gag	gga	ggg	gat		
Ala	Asp	Gly	Lys	Ile	Cys	Leu	Val	Met	Glu	Leu	Ala	Glu	Gly	Gly	Asp		
				85				90				95					
																	336
gtc	ttt	gac	tgc	gtg	ctg	aat	ggg	ggg	cca	ctg	cct	gaa	agc	cgg	gcc		
Val	Phe	Asp	Cys	Val	Leu	Asn	Gly	Gly	Pro	Leu	Pro	Glu	Ser	Arg	Ala		
		100						105				110					
																	384
aag	gcc	ctc	ttc	cgt	cag	atg	gtt	gag	gcc	atc	cgc	tac	tgc	cat	ggc		
Lys	Ala	Leu	Phe	Arg	Gln	Met	Val	Glu	Ala	Ile	Arg	Tyr	Cys	His	Gly		
		115				120						125					

55/155

tgt	ggt	gtg	gcc	cac	cgg	gac	ctc	aaa	tgt	gag	aac	gcc	ttg	ttg	cag	432
Cys	Gly	Val	Ala	His	Arg	Asp	Leu	Lys	Cys	Glu	Asn	Ala	Leu	Leu	Gln	
	130					135					140					
ggc	ttc	aac	ctg	aag	ctg	act	gac	ttt	ggc	ttt	gcc	aag	gtg	ttg	ccc	480
Gly	Phe	Asn	Leu	Lys	Leu	Thr	Asp	Phe	Gly	Phe	Ala	Lys	Val	Leu	Pro	
145					150					155					160	
aag	tca	cac	cgg	gag	ctg	agc	cag	acc	ttc	tgc	ggc	agt	aca	gcc	tat	528
Lys	Ser	His	Arg	Glu	Leu	Ser	Gln	Thr	Phe	Cys	Gly	Ser	Thr	Ala	Tyr	
				165					170					175		
gct	gcc	ccc	gag	gtg	ctg	cag	ggc	att	ccc	cac	gat	agc	aaa	aaa	ggg	576
Ala	Ala	Pro	Glu	Val	Leu	Gln	Gly	Ile	Pro	His	Asp	Ser	Lys	Lys	Gly	
			180					185					190			
gat	gtc	tgg	agc	atg	ggg	gtg	gtc	ctg	tat	gtc	atg	ctc	tgt	gcc	agc	624
Asp	Val	Trp	Ser	Met	Gly	Val	Val	Leu	Tyr	Val	Met	Leu	Cys	Ala	Ser	
	195					200						205				
cta	cct	ttt	gac	gac	aca	gac	atc	ccc	aag	atg	ctg	tgg	cag	cag	cag	672
Leu	Pro	Phe	Asp	Asp	Thr	Asp	Ile	Pro	Lys	Met	Leu	Trp	Gln	Gln	Gln	
	210					215					220					
aag	ggg	gtg	tcc	ttc	ccc	act	cat	ctg	agc	atc	tgc	gcc	gat	tgc	cag	720
Lys	Gly	Val	Ser	Phe	Pro	Thr	His	Leu	Ser	Ile	Ser	Ala	Asp	Cys	Gln	
225					230					235					240	
gac	ctg	ctc	aag	agg	ctc	ctg	gaa	ccc	gat	atg	atc	ctc	cgg	cct	tca	768
Asp	Leu	Leu	Lys	Arg	Leu	Leu	Glu	Pro	Asp	Met	Ile	Leu	Arg	Pro	Ser	
				245					250					255		
att	gaa	gaa	gtt	aag	cag	cat	cgc	tgg	ttt	caa	act	cct	gac	ctc	aat	816
Ile	Glu	Glu	Val	Lys	Gln	His	Arg	Trp	Phe	Gln	Thr	Pro	Asp	Leu	Asn	
			260					265					270			
gat	ctg	gcc	acc	tgc	gcc	tcc	caa	gat	act	ggg	cat	aga	aag	cac	cct	864
Asp	Leu	Ala	Thr	Ser	Ala	Ser	Gln	Asp	Thr	Gly	His	Arg	Lys	His	Pro	
		275					280					285				
ttc	tct	gcc	agg	ata	ctc	agt	caa	cca	caa	tcc	agc	ttc	tcc	ctt	gaa	912
Phe	Ser	Ala	Arg	Ile	Leu	Ser	Gln	Pro	Gln	Ser	Ser	Phe	Ser	Leu	Glu	
	290					295					300					
att	cag	aat	gct	gag	ctg	gct	tct	cct	gct	cac	tgg	ggg	aaa	gtt	cag	960
Ile	Gln	Asn	Ala	Glu	Leu	Ala	Ser	Pro	Ala	His	Trp	Gly	Lys	Val	Gln	
305					310					315					320	
cct	cca	cag	gag	gac	ctg	gag	gct	cag	ctg	ggg	tcc	ctt	ggg	ggg	ttg	1008
Pro	Pro	Gln	Glu	Asp	Leu	Glu	Ala	Gln	Leu	Gly	Ser	Leu	Gly	Gly	Leu	
				325					330				335			
cag	aag	gtt	tgc	tct	cct	cag	ggg	gct	ctg	gtg	tct	gag	ctg	gca	atg	1056
Gln	Lys	Val	Ser	Ser	Pro	Gln	Gly	Ala	Leu	Val	Ser	Glu	Leu	Ala	Met	
			340				345						350			
gag	atg	caa	tcc	tat	tat	gcc	aag	ctt	ttg	ggg	gag	ctg	aat	gaa	cag	1104
Glu	Met	Gln	Ser	Tyr	Tyr	Ala	Lys	Leu	Leu	Gly	Glu	Leu	Asn	Glu	Gln	
		355					360					365				

56/155

aga	aag	agg	gac	ttt	ttc	tgt	gac	tgc	agc	atc	att	gtg	gaa	ggg	cgg	1152
Arg	Lys	Arg	Asp	Phe	Phe	Cys	Asp	Cys	Ser	Ile	Ile	Val	Glu	Gly	Arg	
	370					375					380					
atc	ttc	aag	gcc	cac	agg	aac	att	ttg	ttt	gct	aac	agc	ggc	tac	ttc	1200
Ile	Phe	Lys	Ala	His	Arg	Asn	Ile	Leu	Phe	Ala	Asn	Ser	Gly	Tyr	Phe	
385					390					395					400	
cga	gcc	ctg	ctc	att	cac	tat	atc	cag	gac	agc	ggg	cgg	cat	agc	acc	1248
Arg	Ala	Leu	Leu	Ile	His	Tyr	Ile	Gln	Asp	Ser	Gly	Arg	His	Ser	Thr	
				405					410					415		
gcc	tcc	ttg	gac													1260
Ala	Ser	Leu	Asp													
			420													

<210> 34
 <211> 420
 <212> PRT
 <213> Homo sapiens

<400> 34
 Ser Met Glu Asp Phe Leu Leu Ser Asn Gly Tyr Gln Leu Gly Lys Thr
 1 5 10 15
 Ile Gly Glu Gly Thr Tyr Ser Lys Val Lys Glu Ala Phe Ser Lys Lys
 20 25 30
 His Gln Arg Lys Val Ala Ile Lys Val Ile Asp Lys Met Gly Gly Pro
 35 40 45
 Glu Glu Phe Ile Gln Arg Phe Leu Pro Arg Glu Leu Gln Ile Val Arg
 50 55 60
 Thr Leu Asp His Lys Asn Ile Ile Gln Val Tyr Glu Met Leu Glu Ser
 65 70 75 80
 Ala Asp Gly Lys Ile Cys Leu Val Met Glu Leu Ala Glu Gly Gly Asp
 85 90 95
 Val Phe Asp Cys Val Leu Asn Gly Gly Pro Leu Pro Glu Ser Arg Ala
 100 105 110
 Lys Ala Leu Phe Arg Gln Met Val Glu Ala Ile Arg Tyr Cys His Gly
 115 120 125
 Cys Gly Val Ala His Arg Asp Leu Lys Cys Glu Asn Ala Leu Leu Gln
 130 135 140
 Gly Phe Asn Leu Lys Leu Thr Asp Phe Gly Phe Ala Lys Val Leu Pro
 145 150 155 160
 Lys Ser His Arg Glu Leu Ser Gln Thr Phe Cys Gly Ser Thr Ala Tyr
 165 170 175
 Ala Ala Pro Glu Val Leu Gln Gly Ile Pro His Asp Ser Lys Lys Gly
 180 185 190
 Asp Val Trp Ser Met Gly Val Val Leu Tyr Val Met Leu Cys Ala Ser
 195 200 205
 Leu Pro Phe Asp Asp Thr Asp Ile Pro Lys Met Leu Trp Gln Gln Gln
 210 215 220
 Lys Gly Val Ser Phe Pro Thr His Leu Ser Ile Ser Ala Asp Cys Gln
 225 230 235 240
 Asp Leu Leu Lys Arg Leu Leu Glu Pro Asp Met Ile Leu Arg Pro Ser
 245 250 255
 Ile Glu Glu Val Lys Gln His Arg Trp Phe Gln Thr Pro Asp Leu Asn
 260 265 270
 Asp Leu Ala Thr Ser Ala Ser Gln Asp Thr Gly His Arg Lys His Pro
 275 280 285
 Phe Ser Ala Arg Ile Leu Ser Gln Pro Gln Ser Ser Phe Ser Leu Glu
 290 295 300

57/155

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Ile Gln Asn Ala Glu Leu Ala Ser Pro Ala His Trp Gly Lys Val Gln
305          310          315          320
Pro Pro Gln Glu Asp Leu Glu Ala Gln Leu Gly Ser Leu Gly Gly Leu
          325          330          335
Gln Lys Val Ser Ser Pro Gln Gly Ala Leu Val Ser Glu Leu Ala Met
          340          345          350
Glu Met Gln Ser Tyr Tyr Ala Lys Leu Leu Gly Glu Leu Asn Glu Gln
          355          360          365
Arg Lys Arg Asp Phe Phe Cys Asp Cys Ser Ile Ile Val Glu Gly Arg
          370          375          380
Ile Phe Lys Ala His Arg Asn Ile Leu Phe Ala Asn Ser Gly Tyr Phe
385          390          395          400
Arg Ala Leu Leu Ile His Tyr Ile Gln Asp Ser Gly Arg His Ser Thr
          405          410          415
Ala Ser Leu Asp
          420

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<210> 35
<211> 1128
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1) ... (1128)
<223> MOOSE03332

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<400> 35
aag ctt tac aaa tta gag aga tcg tac att agc aag cta acc cta ggg 48
Lys Leu Tyr Lys Leu Glu Arg Ser Tyr Ile Ser Lys Leu Thr Leu Gly
1          5          10          15

caa tta cat ttt gga aaa ggg cgt ttc ggc cag gtt cac aag tgt gag 96
Gln Leu His Phe Gly Lys Gly Arg Phe Gly Gln Val His Lys Cys Glu
          20          25          30

gag acg gcc aca ggt ctg aag ctg gca gcc aaa atc atc aag acc aga 144
Glu Thr Ala Thr Gly Leu Lys Leu Ala Ala Lys Ile Ile Lys Thr Arg
          35          40          45

ggc atg aag gac aag gta cag cct gag gag gtg aag aac gag atc agc 192
Gly Met Lys Asp Lys Val Gln Pro Glu Glu Val Lys Asn Glu Ile Ser
          50          55          60

gtc atg aac cag ctg gac cac gcg aac ctc atc cag ctg tac gat gcc 240
Val Met Asn Gln Leu Asp His Ala Asn Leu Ile Gln Leu Tyr Asp Ala
65          70          75          80

ttc gag tct aag aac gac att gtc ctg gtc atg gag tat gtg gat ggt 288
Phe Glu Ser Lys Asn Asp Ile Val Leu Val Met Glu Tyr Val Asp Gly
          85          90          95

ggg gag ctg ttt gac cgc atc atc gat gag agc tac aat ttg acg gag 336
Gly Glu Leu Phe Asp Arg Ile Ile Asp Glu Ser Tyr Asn Leu Thr Glu
          100          105          110

ctt gat acc atc ctg ttc atg aag cag ata tgt gag ggg ata agg cac 384
Leu Asp Thr Ile Leu Phe Met Lys Gln Ile Cys Glu Gly Ile Arg His
          115          120          125

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58/155

atg	cat	cag	atg	tac	att	ctc	cac	ttg	gac	ctg	aag	cct	gag	aat	atc	432
Met	His	Gln	Met	Tyr	Ile	Leu	His	Leu	Asp	Leu	Lys	Pro	Glu	Asn	Ile	
	130					135					140					
ctg	tgt	gtg	aat	cgg	gat	gct	aag	caa	ata	aaa	att	att	gat	ttt	gga	480
Leu	Cys	Val	Asn	Arg	Asp	Ala	Lys	Gln	Ile	Lys	Ile	Ile	Asp	Phe	Gly	
145					150					155					160	
ttg	gcc	aga	agg	tat	aag	ctg	aag	gtg	aac	ttt	gga	acc	cca	gaa	ttt	528
Leu	Ala	Arg	Arg	Tyr	Lys	Leu	Lys	Val	Asn	Phe	Gly	Thr	Pro	Glu	Phe	
				165					170					175		
ctc	gcc	cct	gaa	gtt	gtg	aac	tat	gat	ttt	gtt	tca	ttt	ccc	act	gac	576
Leu	Ala	Pro	Glu	Val	Val	Asn	Tyr	Asp	Phe	Val	Ser	Phe	Pro	Thr	Asp	
			180					185					190			
atg	tgg	agt	gtg	ggg	gtc	atc	gcc	tat	atg	cta	ctt	agc	ggg	ttg	tcg	624
Met	Trp	Ser	Val	Gly	Val	Ile	Ala	Tyr	Met	Leu	Leu	Ser	Gly	Leu	Ser	
	195						200					205				
cct	ttc	ctg	ggg	gac	aat	gat	gct	gag	acg	ctg	aac	aac	atc	ctg	gcc	672
Pro	Phe	Leu	Gly	Asp	Asn	Asp	Ala	Glu	Thr	Leu	Asn	Asn	Ile	Leu	Ala	
	210					215					220					
tgc	agg	tgg	gac	tta	gag	gat	gaa	gaa	ttt	cag	gac	atc	tcg	gag	gag	720
Cys	Arg	Trp	Asp	Leu	Glu	Asp	Glu	Glu	Phe	Gln	Asp	Ile	Ser	Glu	Glu	
225					230					235					240	
gcc	aag	gag	ttc	atc	tct	aag	ctt	ctg	att	aag	gag	aag	agt	tgg	cga	768
Ala	Lys	Glu	Phe	Ile	Ser	Lys	Leu	Leu	Ile	Lys	Glu	Lys	Ser	Trp	Arg	
				245					250					255		
ata	agt	gca	agc	gaa	gct	ctc	aag	cac	ccc	tgg	ttg	tca	gac	cac	aag	816
Ile	Ser	Ala	Ser	Glu	Ala	Leu	Lys	His	Pro	Trp	Leu	Ser	Asp	His	Lys	
				260				265					270			
ctc	cac	tcc	aga	ctc	aat	gcc	cag	gtg	acc	acg	gct	tct	tgc	tct	tcc	864
Leu	His	Ser	Arg	Leu	Asn	Ala	Gln	Val	Thr	Thr	Ala	Ser	Cys	Ser	Ser	
				275			280					285				
tct	ttt	tct	cct	cgg	ggc	ctg	cgg	gcg	cgg	cgt	ggc	ggg	gcg	gga	aaa	912
Ser	Phe	Ser	Pro	Arg	Gly	Leu	Arg	Ala	Arg	Arg	Gly	Gly	Ala	Gly	Lys	
	290					295					300					
cgg	ctc	tgt	ccc	gtg	ggg	cgc	agg	cag	gaa	cgg	att	gcc	cag	gaa	ggg	960
Arg	Leu	Cys	Pro	Val	Gly	Arg	Arg	Gln	Glu	Arg	Ile	Ala	Gln	Glu	Gly	
305					310					315					320	
atg	gag	gac	cga	aaa	tgg	atc	acc	agc	cct	cat	gga	caa	ctt	aaa	cta	1008
Met	Glu	Asp	Arg	Lys	Trp	Ile	Thr	Ser	Pro	His	Gly	Gln	Leu	Lys	Leu	
				325					330					335		
aag	gtg	gaa	aag	aca	gaa	aag	ctg	gca	ggg	gga	att	gtc	tcc	agc	caa	1056
Lys	Val	Glu	Lys	Thr	Glu	Lys	Leu	Ala	Gly	Gly	Ile	Val	Ser	Ser	Gln	
				340				345					350			
cct	gtc	aac	ttt	tgg	aaa	aag	atg	gat	cac	aaa	gaa	tgg	gaa	gtg	gaa	1104
Pro	Val	Asn	Phe	Trp	Lys	Lys	Met	Asp	His	Lys	Glu	Trp	Glu	Val	Glu	
		355					360					365				

59/155

gag aag gag agg aga aac caa gaa
 Glu Lys Glu Arg Arg Asn Gln Glu
 370 375

1128

<210> 36
 <211> 376
 <212> PRT
 <213> Homo sapiens

<400> 36
 Lys Leu Tyr Lys Leu Glu Arg Ser Tyr Ile Ser Lys Leu Thr Leu Gly
 1 5 10 15
 Gln Leu His Phe Gly Lys Gly Arg Phe Gly Gln Val His Lys Cys Glu
 20 25 30
 Glu Thr Ala Thr Gly Leu Lys Leu Ala Ala Lys Ile Ile Lys Thr Arg
 35 40 45
 Gly Met Lys Asp Lys Val Gln Pro Glu Glu Val Lys Asn Glu Ile Ser
 50 55 60
 Val Met Asn Gln Leu Asp His Ala Asn Leu Ile Gln Leu Tyr Asp Ala
 65 70 75 80
 Phe Glu Ser Lys Asn Asp Ile Val Leu Val Met Glu Tyr Val Asp Gly
 85 90 95
 Gly Glu Leu Phe Asp Arg Ile Ile Asp Glu Ser Tyr Asn Leu Thr Glu
 100 105 110
 Leu Asp Thr Ile Leu Phe Met Lys Gln Ile Cys Glu Gly Ile Arg His
 115 120 125
 Met His Gln Met Tyr Ile Leu His Leu Asp Leu Lys Pro Glu Asn Ile
 130 135 140
 Leu Cys Val Asn Arg Asp Ala Lys Gln Ile Lys Ile Ile Asp Phe Gly
 145 150 155 160
 Leu Ala Arg Arg Tyr Lys Leu Lys Val Asn Phe Gly Thr Pro Glu Phe
 165 170 175
 Leu Ala Pro Glu Val Val Asn Tyr Asp Phe Val Ser Phe Pro Thr Asp
 180 185 190
 Met Trp Ser Val Gly Val Ile Ala Tyr Met Leu Leu Ser Gly Leu Ser
 195 200 205
 Pro Phe Leu Gly Asp Asn Asp Ala Glu Thr Leu Asn Asn Ile Leu Ala
 210 215 220
 Cys Arg Trp Asp Leu Glu Asp Glu Glu Phe Gln Asp Ile Ser Glu Glu
 225 230 235 240
 Ala Lys Glu Phe Ile Ser Lys Leu Leu Ile Lys Glu Lys Ser Trp Arg
 245 250 255
 Ile Ser Ala Ser Glu Ala Leu Lys His Pro Trp Leu Ser Asp His Lys
 260 265 270
 Leu His Ser Arg Leu Asn Ala Gln Val Thr Thr Ala Ser Cys Ser Ser
 275 280 285
 Ser Phe Ser Pro Arg Gly Leu Arg Ala Arg Arg Gly Gly Ala Gly Lys
 290 295 300
 Arg Leu Cys Pro Val Gly Arg Arg Gln Glu Arg Ile Ala Gln Glu Gly
 305 310 315 320
 Met Glu Asp Arg Lys Trp Ile Thr Ser Pro His Gly Gln Leu Lys Leu
 325 330 335
 Lys Val Glu Lys Thr Glu Lys Leu Ala Gly Gly Ile Val Ser Ser Gln
 340 345 350
 Pro Val Asn Phe Trp Lys Lys Met Asp His Lys Glu Trp Glu Val Glu
 355 360 365
 Glu Lys Glu Arg Arg Asn Gln Glu
 370 375

<210> 37

60/155

<211> 1230

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1230)

<223> MOOSE03340

<400> 37

aaa aca aag caa aac aaa aca aaa caa aga ctc tac ctg ggg ctt ggc	48
Lys Thr Lys Gln Asn Lys Thr Lys Gln Arg Leu Tyr Leu Gly Leu Gly	
1 5 10 15	
aag ttt ggg gca gtc tgt acc tgc atg gag aaa gcc aca ggc ctc aag	96
Lys Phe Gly Ala Val Cys Thr Cys Met Glu Lys Ala Thr Gly Leu Lys	
20 25 30	
ctg gca gcc aag gtc atc aag aaa cag act ccc aaa gac aag gta gaa	144
Leu Ala Ala Lys Val Ile Lys Lys Gln Thr Pro Lys Asp Lys Val Glu	
35 40 45	
atg gtg ttg ctg gag att gag gtc atg aac cag ctg aac cac cgc aat	192
Met Val Leu Leu Glu Ile Glu Val Met Asn Gln Leu Asn His Arg Asn	
50 55 60	
ctg atc cag ctg tat gca gcc atc gag act ccg cat gag atc gtc ctg	240
Leu Ile Gln Leu Tyr Ala Ala Ile Glu Thr Pro His Glu Ile Val Leu	
65 70 75 80	
ttc atg gag tac atc gag ggc gga gag ctc ttc gag agg att gtg gat	288
Phe Met Glu Tyr Ile Glu Gly Gly Glu Leu Phe Glu Arg Ile Val Asp	
85 90 95	
gag gac tac cat ctg acc gag gtg gac acc atg gtg ttt gtc agg cag	336
Glu Asp Tyr His Leu Thr Glu Val Asp Thr Met Val Phe Val Arg Gln	
100 105 110	
atc tgt gac ggg atc ctc ttc atg cac aag atg agg gtt ttg cac ctg	384
Ile Cys Asp Gly Ile Leu Phe Met His Lys Met Arg Val Leu His Leu	
115 120 125	
gac ctc aag cca gag aac atc ctg tgt gtc aac acc acc ggg cat ttg	432
Asp Leu Lys Pro Glu Asn Ile Leu Cys Val Asn Thr Thr Gly His Leu	
130 135 140	
gtg aag atc att gac ttt ggc ctg gca cgg agg tac cac ctg ggt ggg	480
Val Lys Ile Ile Asp Phe Gly Leu Ala Arg Arg Tyr His Leu Gly Gly	
145 150 155 160	
tgg gga ggg caa gac aag cct ctg agt tgg cag ggg aca ggg gtg ggg	528
Trp Gly Gly Gln Asp Lys Pro Leu Ser Trp Gln Gly Thr Gly Val Gly	
165 170 175	
tgg agg ggg cat ggg tat agg cca gga gct gtg ctc tca gcc ctt ggt	576
Trp Arg Gly His Gly Tyr Arg Pro Gly Ala Val Leu Ser Ala Leu Gly	
180 185 190	
ctc acc ccc agg tat aac ccc aac gag aag ctg aag gtg aac ttt ggg	624
Leu Thr Pro Arg Tyr Asn Pro Asn Glu Lys Leu Lys Val Asn Phe Gly	
195 200 205	

61/155

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acc cca gag ttc ctg tca cct gag gtg gtg aat tat gac caa atc tcc 672
Thr Pro Glu Phe Leu Ser Pro Glu Val Val Asn Tyr Asp Gln Ile Ser
210 215 220

gat aag aca gac atg tgg agt atg ggg gtg atc acc tac atg ctg ctg 720
Asp Lys Thr Asp Met Trp Ser Met Gly Val Ile Thr Tyr Met Leu Leu
225 230 235 240

agc ggc ctc tcc ccc ttc ctg gga gat gat gac aca gag acc cta aac 768
Ser Gly Leu Ser Pro Phe Leu Gly Asp Asp Asp Thr Glu Thr Leu Asn
245 250 255

aac gtt cta tct ggc aac tgg tac ttt gat gaa gag acc ttt gag gcc 816
Asn Val Leu Ser Gly Asn Trp Tyr Phe Asp Glu Glu Thr Phe Glu Ala
260 265 270

gta tca gac gag gcc aaa gac ttt gtc tcc aac ctc atc gtc aag gac 864
Val Ser Asp Glu Ala Lys Asp Phe Val Ser Asn Leu Ile Val Lys Asp
275 280 285

cag agg gcc cgg atg aac gct gcc cag tgt ctc gcc cat ccc tgg ctc 912
Gln Arg Ala Arg Met Asn Ala Ala Gln Cys Leu Ala His Pro Trp Leu
290 295 300

aac aac ctg gcg gag aaa gcc aaa cgc tgt aac cga cgc ctt aag tcc 960
Asn Asn Leu Ala Glu Lys Ala Lys Arg Cys Asn Arg Arg Leu Lys Ser
305 310 315 320

cag atc ttg ctt aag aaa tac ctc atg aag agg cgc tgg aag gta ccg 1008
Gln Ile Leu Leu Lys Lys Tyr Leu Met Lys Arg Arg Trp Lys Val Pro
325 330 335

ctg gat tca gga aag aaa gaa aga gag aga gag aaa gaa aga aag aaa 1056
Leu Asp Ser Gly Lys Lys Glu Arg Glu Arg Glu Lys Glu Arg Lys Lys
340 345 350

gaa aga aag aaa gaa aga aag aaa gaa aga aag aaa aag gaa gga agg 1104
Glu Arg Lys Lys Glu Arg Lys Lys Glu Arg Lys Lys Lys Glu Gly Arg
355 360 365

aag aaa gaa aga aag aaa gag aaa gaa aga aag aaa aag aaa gaa agg 1152
Lys Lys Glu Arg Lys Lys Glu Lys Glu Arg Lys Lys Lys Lys Glu Arg
370 375 380

aag gaa gga agg aag gaa gga agg aag aaa gaa aga aag aaa gaa aga 1200
Lys Glu Gly Arg Lys Glu Gly Arg Lys Lys Glu Arg Lys Lys Glu Arg
385 390 395 400

aag aaa gaa aga aag aaa gaa aga aag aaa
Lys Lys Glu Arg Lys Lys Glu Arg Lys Lys
405 410

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<210> 38
<211> 410
<212> PRT
<213> Homo sapiens

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<400> 38
Lys Thr Lys Gln Asn Lys Thr Lys Gln Arg Leu Tyr Leu Gly Leu Gly
1 5 10 15

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62/155

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Lys Phe Gly Ala Val Cys Thr Cys Met Glu Lys Ala Thr Gly Leu Lys
      20      25      30
Leu Ala Ala Lys Val Ile Lys Lys Gln Thr Pro Lys Asp Lys Val Glu
      35      40      45
Met Val Leu Leu Glu Ile Glu Val Met Asn Gln Leu Asn His Arg Asn
      50      55      60
Leu Ile Gln Leu Tyr Ala Ile Glu Thr Pro His Glu Ile Val Leu
      65      70      75      80
Phe Met Glu Tyr Ile Glu Gly Gly Glu Leu Phe Glu Arg Ile Val Asp
      85      90      95
Glu Asp Tyr His Leu Thr Glu Val Asp Thr Met Val Phe Val Arg Gln
      100      105      110
Ile Cys Asp Gly Ile Leu Phe Met His Lys Met Arg Val Leu His Leu
      115      120      125
Asp Leu Lys Pro Glu Asn Ile Leu Cys Val Asn Thr Thr Gly His Leu
      130      135      140
Val Lys Ile Ile Asp Phe Gly Leu Ala Arg Arg Tyr His Leu Gly Gly
      145      150      155      160
Trp Gly Gly Gln Asp Lys Pro Leu Ser Trp Gln Gly Thr Gly Val Gly
      165      170      175
Trp Arg Gly His Gly Tyr Arg Pro Gly Ala Val Leu Ser Ala Leu Gly
      180      185      190
Leu Thr Pro Arg Tyr Asn Pro Asn Glu Lys Leu Lys Val Asn Phe Gly
      195      200      205
Thr Pro Glu Phe Leu Ser Pro Glu Val Val Asn Tyr Asp Gln Ile Ser
      210      215      220
Asp Lys Thr Asp Met Trp Ser Met Gly Val Ile Thr Tyr Met Leu Leu
      225      230      235      240
Ser Gly Leu Ser Pro Phe Leu Gly Asp Asp Asp Thr Glu Thr Leu Asn
      245      250      255
Asn Val Leu Ser Gly Asn Trp Tyr Phe Asp Glu Glu Thr Phe Glu Ala
      260      265      270
Val Ser Asp Glu Ala Lys Asp Phe Val Ser Asn Leu Ile Val Lys Asp
      275      280      285
Gln Arg Ala Arg Met Asn Ala Ala Gln Cys Leu Ala His Pro Trp Leu
      290      295      300
Asn Asn Leu Ala Glu Lys Ala Lys Arg Cys Asn Arg Arg Leu Lys Ser
      305      310      315      320
Gln Ile Leu Leu Lys Lys Tyr Leu Met Lys Arg Arg Trp Lys Val Pro
      325      330      335
Leu Asp Ser Gly Lys Lys Glu Arg Glu Arg Glu Lys Glu Arg Lys Lys
      340      345      350
Glu Arg Lys Lys Glu Arg Lys Lys Glu Arg Lys Lys Lys Glu Gly Arg
      355      360      365
Lys Lys Glu Arg Lys Lys Glu Lys Glu Arg Lys Lys Lys Lys Glu Arg
      370      375      380
Lys Glu Gly Arg Lys Glu Gly Arg Lys Lys Glu Arg Lys Lys Glu Arg
      385      390      395      400
Lys Lys Glu Arg Lys Lys Glu Arg Lys Lys
      405      410

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<210> 39

<211> 1239

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1239)

<223> MOOSE03350

63/155

<400> 39
 agg aga cac aac ccc agg cag tgc gaa ctc ggt tat aag ctg ggc cgc 48
 Arg Arg His Asn Pro Arg Gln Cys Glu Leu Gly Tyr Lys Leu Gly Arg
 1 5 10 15

aca att gga gag ggc agc tac tcc aag gtg aag gtg gcc aca tcc aag 96
 Thr Ile Gly Glu Gly Ser Tyr Ser Lys Val Lys Val Ala Thr Ser Lys
 20 25 30

aag tac aag ggt acc gtg gcc atc aag gtg gtg gac cgg cgg cga gcg 144
 Lys Tyr Lys Gly Thr Val Ala Ile Lys Val Val Asp Arg Arg Arg Ala
 35 40 45

ccc ccg gac ttc gtc aac aag ttc ctg ccg cga gag ctg tcc atc ctg 192
 Pro Pro Asp Phe Val Asn Lys Phe Leu Pro Arg Glu Leu Ser Ile Leu
 50 55 60

cgg ggc gtg cga cac ccg cac atc gtg cac gtc ttc gag ttc atc gag 240
 Arg Gly Val Arg His Pro His Ile Val His Val Phe Glu Phe Ile Glu
 65 70 75 80

gtg tgc aac ggg aaa ctg tac atc gtg atg gaa gcg gcc gcc acc gac 288
 Val Cys Asn Gly Lys Leu Tyr Ile Val Met Glu Ala Ala Ala Thr Asp
 85 90 95

ctg ctg caa gcc gtg cag cgc aac ggg cgc atc ccc gga gtt cag gcg 336
 Leu Leu Gln Ala Val Gln Arg Asn Gly Arg Ile Pro Gly Val Gln Ala
 100 105 110

cgc gac ctc ttt gcg cag atc gcc ggc gcc gtg cgc tac ctg cac gat 384
 Arg Asp Leu Phe Ala Gln Ile Ala Gly Ala Val Arg Tyr Leu His Asp
 115 120 125

cat cac ctg gtg cac cgc gac ctc aag tgc gaa aac gtg ctg ctg agc 432
 His His Leu Val His Arg Asp Leu Lys Cys Glu Asn Val Leu Leu Ser
 130 135 140

ccg gac gag cgc cgc gtc aag ctc acc gac ttc ggc ttc ggc cgc cag 480
 Pro Asp Glu Arg Arg Val Lys Leu Thr Asp Phe Gly Phe Gly Arg Gln
 145 150 155 160

gcc cat ggc tac cca gac ctg agc acc acc tac tgc ggc tca gcc gcc 528
 Ala His Gly Tyr Pro Asp Leu Ser Thr Thr Tyr Cys Gly Ser Ala Ala
 165 170 175

tac gcg tca ccc gag gtg ctc ctg ggc atc ccc tac gac ccc aag aag 576
 Tyr Ala Ser Pro Glu Val Leu Leu Gly Ile Pro Tyr Asp Pro Lys Lys
 180 185 190

tac gat gtg tgg agc atg ggc gtc gtg ctc tac gtc atg gtc acc ggg 624
 Tyr Asp Val Trp Ser Met Gly Val Val Leu Tyr Val Met Val Thr Gly
 195 200 205

tgc atg ccc ttc gac gac tcg gac atc gcc ggc ctg ccc cgg cgc cag 672
 Cys Met Pro Phe Asp Asp Ser Asp Ile Ala Gly Leu Pro Arg Arg Gln
 210 215 220

aaa cgc ggc gtg ctc tat ccc gaa ggc ctc gag ctg tcc gag cgc tgc 720
 Lys Arg Gly Val Leu Tyr Pro Glu Gly Leu Glu Leu Ser Glu Arg Cys
 225 230 235 240

64/155

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aag gcc ctg atc gcc gag ctg ctg cag ttc agc ccg tcc gcc agg ccc 768
Lys Ala Leu Ile Ala Glu Leu Leu Gln Phe Ser Pro Ser Ala Arg Pro
245 250 255

tcc gcg ggc cag ggc tgc ctc ggc cat ccc tgc atc tgt cag tca aga 816
Ser Ala Gly Gln Gly Cys Leu Gly His Pro Cys Ile Cys Gln Ser Arg
260 265 270

gag gtt tgc ccc gac agc ctg cgt ccc ctg cac cag gtc cca ttc cca 864
Glu Val Cys Pro Asp Ser Leu Arg Pro Leu His Gln Val Pro Phe Pro
275 280 285

cct cgg aga agg aaa tgg agt tgt ttg ccg gga gct gcc cca agg ctg 912
Pro Arg Arg Arg Lys Trp Ser Cys Leu Pro Gly Ala Ala Pro Arg Leu
290 295 300

ctg agg cag gag aat ggc atg aac ccc ggg ggg cag agc ctg cag gga 960
Leu Arg Gln Glu Asn Gly Met Asn Pro Gly Gly Gln Ser Leu Gln Gly
305 310 315 320

gcc gag atc gtg cca ctg cgc act cca gcc tgg gcg aca gcc aga ctc 1008
Ala Glu Ile Val Pro Leu Arg Thr Pro Ala Trp Ala Thr Ala Arg Leu
325 330 335

cgt ctc aaa aaa aaa aaa aaa aaa gaa aaa aaa aaa aag aaa aag aaa 1056
Arg Leu Lys Lys Lys Lys Lys Lys Glu Lys Lys Lys Lys Lys Lys Lys
340 345 350

aat cct gtg aca gag aaa aag gac aca gtt atc aat gct act ttg agc 1104
Asn Pro Val Thr Glu Lys Lys Asp Thr Val Ile Asn Ala Thr Leu Ser
355 360 365

ccc aaa gtg gcc aag gaa cac aca tcc cag cct gcc ccg tcc aga cca 1152
Pro Lys Val Ala Lys Glu His Thr Ser Gln Pro Ala Pro Ser Arg Pro
370 375 380

tgg ggc agg cct ttg gtc caa gtg ctg ccc cct ccc aca gca gac aag 1200
Trp Gly Arg Pro Leu Val Gln Val Leu Pro Pro Pro Thr Ala Asp Lys
385 390 395 400

cca ctc atg gta caa ggg gag gtg ggg aag aga aga gca 1239
Pro Leu Met Val Glu Gly Glu Val Gly Lys Arg Arg Ala
405 410

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<210> 40

<211> 413

<212> PRT

<213> Homo sapiens

<400> 40

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Arg Arg His Asn Pro Arg Gln Cys Glu Leu Gly Tyr Lys Leu Gly Arg
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Thr Ile Gly Glu Gly Ser Tyr Ser Lys Val Lys Val Ala Thr Ser Lys
20 25 30
Lys Tyr Lys Gly Thr Val Ala Ile Lys Val Val Asp Arg Arg Arg Ala
35 40 45
Pro Pro Asp Phe Val Asn Lys Phe Leu Pro Arg Glu Leu Ser Ile Leu
50 55 60
Arg Gly Val Arg His Pro His Ile Val His Val Phe Glu Phe Ile Glu
65 70 75 80

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65/155

Val Cys Asn Gly Lys Leu Tyr Ile Val Met Glu Ala Ala Ala Thr Asp
 85 90 95
 Leu Leu Gln Ala Val Gln Arg Asn Gly Arg Ile Pro Gly Val Gln Ala
 100 105 110
 Arg Asp Leu Phe Ala Gln Ile Ala Gly Ala Val Arg Tyr Leu His Asp
 115 120 125
 His His Leu Val His Arg Asp Leu Lys Cys Glu Asn Val Leu Leu Ser
 130 135 140
 Pro Asp Glu Arg Arg Val Lys Leu Thr Asp Phe Gly Phe Gly Arg Gln
 145 150 155 160
 Ala His Gly Tyr Pro Asp Leu Ser Thr Thr Tyr Cys Gly Ser Ala Ala
 165 170 175
 Tyr Ala Ser Pro Glu Val Leu Leu Gly Ile Pro Tyr Asp Pro Lys Lys
 180 185 190
 Tyr Asp Val Trp Ser Met Gly Val Val Leu Tyr Val Met Val Thr Gly
 195 200 205
 Cys Met Pro Phe Asp Asp Ser Asp Ile Ala Gly Leu Pro Arg Arg Gln
 210 215 220
 Lys Arg Gly Val Leu Tyr Pro Glu Gly Leu Glu Leu Ser Glu Arg Cys
 225 230 235 240
 Lys Ala Leu Ile Ala Glu Leu Leu Gln Phe Ser Pro Ser Ala Arg Pro
 245 250 255
 Ser Ala Gly Gln Gly Cys Leu Gly His Pro Cys Ile Cys Gln Ser Arg
 260 265 270
 Glu Val Cys Pro Asp Ser Leu Arg Pro Leu His Gln Val Pro Phe Pro
 275 280 285
 Pro Arg Arg Arg Lys Trp Ser Cys Leu Pro Gly Ala Ala Pro Arg Leu
 290 295 300
 Leu Arg Gln Glu Asn Gly Met Asn Pro Gly Gly Gln Ser Leu Gln Gly
 305 310 315 320
 Ala Glu Ile Val Pro Leu Arg Thr Pro Ala Trp Ala Thr Ala Arg Leu
 325 330 335
 Arg Leu Lys Lys Lys Lys Lys Lys Glu Lys Lys Lys Lys Lys Lys Lys
 340 345 350
 Asn Pro Val Thr Glu Lys Lys Asp Thr Val Ile Asn Ala Thr Leu Ser
 355 360 365
 Pro Lys Val Ala Lys Glu His Thr Ser Gln Pro Ala Pro Ser Arg Pro
 370 375 380
 Trp Gly Arg Pro Leu Val Gln Val Leu Pro Pro Pro Thr Ala Asp Lys
 385 390 395 400
 Pro Leu Met Val Gln Gly Glu Val Gly Lys Arg Arg Ala
 405 410

<210> 41
 <211> 2283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(2283)
 <223> MOOSE03368

<400> 41
 agt ttg cgg gcc gcc ccg gga ccc cga cgc ccg tcg gcc gcc tcc tcc 48
 Ser Leu Arg Ala Ala Pro Gly Pro Arg Arg Pro Ser Ala Ala Ser Ser
 1 5 10 15
 tgt acc agc acc tgg ccc agc tgc gcc acc gcg cca gcc ccg gcg cac 96
 Cys Thr Ser Thr Trp Pro Ser Cys Ala Thr Ala Pro Ala Pro Ala His
 20 25 30

66/155

gct	ccc	ggc	ccg	ggg	ccc	gcc	agc	gtc	tcg	cgc	acc	agc	gcc	cac	agc	144
Ala	Pro	Gly	Pro	Gly	Pro	Ala	Ser	Val	Ser	Arg	Thr	Ser	Ala	His	Ser	
		35					40					45				
tcg	cgc	tgc	agg	gcc	tcg	tac	agc	agc	gcc	acc	cgc	tca	ctg	ggt	gcc	192
Ser	Arg	Cys	Arg	Ala	Ser	Tyr	Ser	Ser	Ala	Thr	Arg	Ser	Leu	Gly	Ala	
	50					55					60					
cgt	tgc	cgg	aac	tcc	atc	gcc	tcc	tgt	ccc	gag	gag	cag	ccc	cac	gtg	240
Arg	Cys	Arg	Asn	Ser	Ile	Ala	Ser	Cys	Pro	Glu	Glu	Gln	Pro	His	Val	
	65				70					75					80	
ggc	aac	tac	cgc	ctg	ctg	agg	acc	att	ggg	aag	ggc	aac	ttt	gcc	aaa	288
Gly	Asn	Tyr	Arg	Leu	Leu	Arg	Thr	Ile	Gly	Lys	Gly	Asn	Phe	Ala	Lys	
				85					90					95		
gtc	aag	ctg	gct	cgg	cac	atc	ctc	act	ggt	cgg	gag	ggt	gcc	atc	aag	336
Val	Lys	Leu	Ala	Arg	His	Ile	Leu	Thr	Gly	Arg	Glu	Val	Ala	Ile	Lys	
			100					105					110			
att	atc	gac	aaa	acc	cag	ctg	aat	ccc	agc	agc	ctg	cag	aag	gat	ccc	384
Ile	Ile	Asp	Lys	Thr	Gln	Leu	Asn	Pro	Ser	Ser	Leu	Gln	Lys	Asp	Pro	
		115					120					125				
cca	agc	cac	cca	ccc	tca	ctc	tcc	tct	gtc	ttc	ctt	tct	ggc	cac	gcc	432
Pro	Ser	His	Pro	Pro	Ser	Leu	Ser	Ser	Val	Phe	Leu	Ser	Gly	His	Ala	
		130				135					140					
cag	ctg	ttc	cga	gaa	gtc	cgc	atc	atg	aag	ggc	cta	aac	cac	ccc	aac	480
Gln	Leu	Phe	Arg	Glu	Val	Arg	Ile	Met	Lys	Gly	Leu	Asn	His	Pro	Asn	
	145				150					155					160	
atc	gtg	aag	ctc	ttt	gag	gtg	att	gag	act	gag	aag	acg	ctg	tac	ctg	528
Ile	Val	Lys	Leu	Phe	Glu	Val	Ile	Glu	Thr	Glu	Lys	Thr	Leu	Tyr	Leu	
			165					170					175			
gtg	atg	gag	tac	gca	agt	gct	gga	gaa	gtg	ttt	gac	tac	ctc	gtg	tcg	576
Val	Met	Glu	Tyr	Ala	Ser	Ala	Gly	Glu	Val	Phe	Asp	Tyr	Leu	Val	Ser	
			180				185						190			
cat	ggc	cgc	atg	aag	gag	aag	gaa	gct	cga	gcc	aag	ttc	cga	cag	att	624
His	Gly	Arg	Met	Lys	Glu	Lys	Glu	Ala	Arg	Ala	Lys	Phe	Arg	Gln	Ile	
		195					200					205				
gtt	tcg	gct	gtg	cac	tat	tgt	cac	cag	aaa	aat	att	gta	cac	agg	gac	672
Val	Ser	Ala	Val	His	Tyr	Cys	His	Gln	Lys	Asn	Ile	Val	His	Arg	Asp	
	210					215					220					
ctg	aag	gct	gag	aac	ctc	ttg	ctg	gat	gcc	gag	gcc	aac	atc	aag	att	720
Leu	Lys	Ala	Glu	Asn	Leu	Leu	Leu	Asp	Ala	Glu	Ala	Asn	Ile	Lys	Ile	
	225				230					235					240	
gct	gac	ttt	ggc	ttc	agc	aac	gag	ttc	acg	ctg	gga	tcg	aag	ctg	gac	768
Ala	Asp	Phe	Gly	Phe	Ser	Asn	Glu	Phe	Thr	Leu	Gly	Ser	Lys	Leu	Asp	
			245					250						255		
acg	ttc	tgc	ggg	agc	ccc	cca	tat	gcc	gcc	ccg	gag	ctg	ttt	cag	ggc	816
Thr	Phe	Cys	Gly	Ser	Pro	Pro	Tyr	Ala	Ala	Pro	Glu	Leu	Phe	Gln	Gly	
			260					265					270			

67/155

aag Lys	aag Lys	tac Tyr	gac Asp	ggg Gly	ccg Pro	gag Glu	gtg Val	gac Asp	atc Ile	tgg Trp	agc Ser	ctg Leu	gga Gly	gtc Val	atc Ile	864
		275					280					285				
ctg Leu	tac Tyr	acc Thr	ctc Leu	gtc Val	agc Ser	ggc Gly	tcc Ser	ctg Leu	ccc Pro	ttc Phe	gac Asp	ggg Gly	cac His	aac Asn	ctc Leu	912
		290				295					300					
aag Lys	gag Glu	ctg Leu	cgg Arg	gag Glu	cga Arg	gta Val	ctc Leu	aga Arg	ggg Gly	aag Lys	tac Tyr	cgg Arg	gtc Val	cct Pro	ttc Phe	960
					310					315					320	
tac Tyr	atg Met	tca Ser	aca Thr	gac Asp	tgt Cys	gag Glu	agc Ser	atc Ile	ctg Leu	cgg Arg	aga Arg	ttt Phe	ttg Leu	gtg Val	ctg Leu	1008
				325					330					335		
aac Asn	cca Pro	gct Ala	aaa Lys	cgc Arg	tgt Cys	act Thr	ctc Leu	gag Glu	caa Gln	atc Ile	atg Met	aaa Lys	gac Asp	aaa Lys	tgg Trp	1056
			340					345					350			
atc Ile	aac Asn	atc Ile	ggc Gly	tat Tyr	gag Glu	ggg Gly	gag Glu	gag Glu	ttg Leu	aag Lys	cca Pro	tac Tyr	aca Thr	gag Glu	ccc Pro	1104
		355					360					365				
gag Glu	gag Glu	gac Asp	ttc Phe	ggg Gly	gac Asp	acc Thr	aag Lys	aga Arg	att Ile	gag Glu	gtg Val	atg Met	gtg Val	ggg Gly	atg Met	1152
		370				375					380					
ggc Gly	tac Tyr	aca Thr	cgg Arg	gaa Glu	gaa Glu	atc Ile	aaa Lys	gag Glu	tcc Ser	ttg Leu	acc Thr	agc Ser	cag Gln	aag Lys	tac Tyr	1200
				390						395					400	
aac Asn	gaa Glu	gtg Val	acc Thr	gcc Ala	acc Thr	tac Tyr	ctc Leu	ctg Leu	ctg Leu	ggc Gly	agg Arg	aag Lys	act Thr	gag Glu	cga Arg	1248
				405					410					415		
cac His	cac His	caa Gln	cgg Arg	aac Asn	aag Lys	ttc Phe	cag Gln	caa Gln	agg Arg	cac His	cag Gln	cca Pro	cag Gln	caa Gln	agg Arg	1296
			420				425						430			
gca Ala	gcg Ala	gaa Glu	tcg Ser	cac His	cac His	tgc Cys	act Thr	cca Pro	gcc Ala	tgg Trp	caa Gln	cag Gln	aac Asn	cag Gln	act Thr	1344
		435					440					445				
ttg Leu	tct Ser	caa Gln	aaa Lys	aaa Lys	aaa Lys	aaa Lys	aaa Lys	aaa Lys	gaa Glu	ggg Gly	ggc Gly	cca Pro	tcc Ser	cct Pro	gca Ala	1392
		450				455					460					
ccc Pro	ctg Leu	cac His	ccc Pro	aaa Lys	cgc Arg	agc Ser	ccg Pro	acg Thr	agc Ser	acg Thr	ggg Gly	gag Glu	gcg Ala	gag Glu	ctg Leu	1440
					470					475					480	
aag Lys	gag Glu	gag Glu	cgg Arg	ctg Leu	cca Pro	ggc Gly	cgg Arg	aag Lys	gcg Ala	agc Ser	tgc Cys	agc Ser	acc Thr	gcg Ala	ggg Gly	1488
				485					490					495		
agt Ser	ggg Gly	agt Ser	cga Arg	ggg Gly	ctg Leu	ccc Pro	ccc Pro	tcc Ser	agc Ser	ccc Pro	atg Met	gtc Val	agc Ser	agc Ser	gcc Ala	1536
			500					505					510			

68/155

cac His	aac Asn	ccc Pro	aac Asn	aag Lys	gca Ala	gag Glu	atc Ile	cca Pro	gag Glu	cgg Arg	cgg Arg	aag Lys	gac Asp	agc Ser	acg Thr	1584
		515					520					525				
agc Ser	acc Thr	ccc Pro	gaa Glu	tgt Cys	gaa Glu	gaa Glu	tca Ser	aag Lys	gga Gly	ctg Leu	ggg Gly	ccc Pro	tgg Trp	cct Pro	gcc Ala	1632
		530				535					540					
tca Ser	gtc Val	ccc Pro	cac His	cct Pro	gac Asp	ttg Leu	tct Ser	gtc Val	tct Ser	gcc Ala	cac His	agc Ser	tca Ser	ggc Gly	acc Thr	1680
					550					555					560	
cca Pro	cgg Arg	gtg Val	ccc Pro	cct Pro	gcc Ala	tcc Ser	ccc Pro	tcc Ser	agt Ser	cac His	agc Ser	ctg Leu	gca Ala	ccc Pro	cca Pro	1728
				565					570					575		
tca Ser	ggg Gly	gag Glu	cgg Arg	agc Ser	cgc Arg	ctg Leu	gca Ala	cgt Arg	ggg Gly	tcc Ser	acc Thr	atc Ile	cgc Arg	agc Ser	acc Thr	1776
			580					585					590			
ttc Phe	cat His	ggg Gly	ggc Gly	cag Gln	gtc Val	cgg Arg	gac Asp	cgg Arg	cgg Arg	gca Ala	ggg Gly	ggg Gly	ggg Gly	ggg Gly	ggg Gly	1824
		595					600					605				
ggg Gly	ggg Gly	gtg Val	cag Gln	aat Asn	ggg Gly	ccc Pro	cct Pro	gcc Ala	tct Ser	ccc Pro	aca Thr	ctg Leu	gcc Ala	cat His	gag Glu	1872
		610				615					620					
gct Ala	gca Ala	ccc Pro	ctg Leu	ccc Pro	gcc Ala	ggg Gly	cgg Arg	ccc Pro	cgc Arg	ccc Pro	acc Thr	acc Thr	aac Asn	ctc Leu	ttc Phe	1920
					630					635					640	
acc Thr	aag Lys	ctg Leu	acc Thr	tcc Ser	aaa Lys	ctg Leu	acc Thr	cga Arg	agt Ser	tgc Cys	cat His	cta Leu	cct Pro	tgg Trp	gat Asp	1968
				645					650					655		
caa Gln	acg Thr	gaa Glu	acc Thr	gcc Ala	ccc Pro	cgg Arg	ctg Leu	ctc Leu	cga Arg	ttc Phe	ccc Pro	tgg Trp	agt Ser	gtg Val	aag Lys	2016
			660					665					670			
ctg Leu	acc Thr	agc Ser	tcg Ser	cgc Arg	cct Pro	cct Pro	gag Glu	gcc Ala	ctg Leu	atg Met	gca Ala	gct Ala	ctg Leu	cgc Arg	cag Gln	2064
		675					680					685				
gcc Ala	aca Thr	gca Ala	gcc Ala	gcc Ala	cgc Arg	tgc Cys	cgc Arg	tgc Cys	cgc Arg	cag Gln	cca Pro	cag Gln	ccg Pro	ttc Phe	ctg Leu	2112
		690				695					700					
ctg Leu	gcc Ala	tgc Cys	ctg Leu	cac His	ggg Gly	ggg Gly	gcg Ala	ggc Gly	ggg Gly	ccc Pro	gag Glu	ccc Pro	ctg Leu	tcc Ser	cac His	2160
		705			710					715					720	
ttc Phe	gaa Glu	gtg Val	gag Glu	gtc Val	tgc Cys	cag Gln	ctg Leu	ccc Pro	cgg Arg	cca Pro	ggc Gly	ttg Leu	cgg Arg	gga Gly	gtt Val	2208
				725					730					735		
ctc Leu	ttc Phe	cgc Arg	cgt Arg	gtg Val	gcg Ala	ggc Gly	acc Thr	gcc Ala	ctg Leu	gcc Ala	ttc Phe	cgc Arg	acc Thr	ctc Leu	gtc Val	2256
			740					745					750			

69/155

acc cgc atc tcc aac gac ctc gag ctc
 Thr Arg Ile Ser Asn Asp Leu Glu Leu
 755 760

2283

<210> 42
 <211> 761
 <212> PRT
 <213> Homo sapiens

<400> 42
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 1 5 10 15
 Cys Thr Ser Thr Trp Pro Ser Cys Ala Thr Ala Pro Ala Pro Ala His
 20 25 30
 Ala Pro Gly Pro Gly Pro Ala Ser Val Ser Arg Thr Ser Ala His Ser
 35 40 45
 Ser Arg Cys Arg Ala Ser Tyr Ser Ser Ala Thr Arg Ser Leu Gly Ala
 50 55 60
 Arg Cys Arg Asn Ser Ile Ala Ser Cys Pro Glu Glu Gln Pro His Val
 65 70 75 80
 Gly Asn Tyr Arg Leu Leu Arg Thr Ile Gly Lys Gly Asn Phe Ala Lys
 85 90 95
 Val Lys Leu Ala Arg His Ile Leu Thr Gly Arg Glu Val Ala Ile Lys
 100 105 110
 Ile Ile Asp Lys Thr Gln Leu Asn Pro Ser Ser Leu Gln Lys Asp Pro
 115 120 125
 Pro Ser His Pro Pro Ser Leu Ser Ser Val Phe Leu Ser Gly His Ala
 130 135 140
 Gln Leu Phe Arg Glu Val Arg Ile Met Lys Gly Leu Asn His Pro Asn
 145 150 155 160
 Ile Val Lys Leu Phe Glu Val Ile Glu Thr Glu Lys Thr Leu Tyr Leu
 165 170 175
 Val Met Glu Tyr Ala Ser Ala Gly Glu Val Phe Asp Tyr Leu Val Ser
 180 185 190
 His Gly Arg Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile
 195 200 205
 Val Ser Ala Val His Tyr Cys His Gln Lys Asn Ile Val His Arg Asp
 210 215 220
 Leu Lys Ala Glu Asn Leu Leu Leu Asp Ala Glu Ala Asn Ile Lys Ile
 225 230 235 240
 Ala Asp Phe Gly Phe Ser Asn Glu Phe Thr Leu Gly Ser Lys Leu Asp
 245 250 255
 Thr Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe Gln Gly
 260 265 270
 Lys Lys Tyr Asp Gly Pro Glu Val Asp Ile Trp Ser Leu Gly Val Ile
 275 280 285
 Leu Tyr Thr Leu Val Ser Gly Ser Leu Pro Phe Asp Gly His Asn Leu
 290 295 300
 Lys Glu Leu Arg Glu Arg Val Leu Arg Gly Lys Tyr Arg Val Pro Phe
 305 310 315 320
 Tyr Met Ser Thr Asp Cys Glu Ser Ile Leu Arg Arg Phe Leu Val Leu
 325 330 335
 Asn Pro Ala Lys Arg Cys Thr Leu Glu Gln Ile Met Lys Asp Lys Trp
 340 345 350
 Ile Asn Ile Gly Tyr Glu Gly Glu Glu Leu Lys Pro Tyr Thr Glu Pro
 355 360 365
 Glu Glu Asp Phe Gly Asp Thr Lys Arg Ile Glu Val Met Val Gly Met
 370 375 380
 Gly Tyr Thr Arg Glu Glu Ile Lys Glu Ser Leu Thr Ser Gln Lys Tyr
 385 390 395 400

70/155

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Asn Glu Val Thr Ala Thr Tyr Leu Leu Leu Gly Arg Lys Thr Glu Arg
      405      410      415
His His Gln Arg Asn Lys Phe Gln Gln Arg His Gln Pro Gln Gln Arg
      420      425      430
Ala Ala Glu Ser His His Cys Thr Pro Ala Trp Gln Gln Asn Gln Thr
      435      440      445
Leu Ser Gln Lys Lys Lys Lys Lys Glu Gly Gly Pro Ser Pro Ala
      450      455      460
Pro Leu His Pro Lys Arg Ser Pro Thr Ser Thr Gly Glu Ala Glu Leu
465      470      475      480
Lys Glu Glu Arg Leu Pro Gly Arg Lys Ala Ser Cys Ser Thr Ala Gly
      485      490      495
Ser Gly Ser Arg Gly Leu Pro Pro Ser Ser Pro Met Val Ser Ser Ala
      500      505      510
His Asn Pro Asn Lys Ala Glu Ile Pro Glu Arg Arg Lys Asp Ser Thr
      515      520      525
Ser Thr Pro Glu Cys Glu Glu Ser Lys Gly Leu Gly Pro Trp Pro Ala
      530      535      540
Ser Val Pro His Pro Asp Leu Ser Val Ser Ala His Ser Ser Gly Thr
545      550      555      560
Pro Arg Val Pro Pro Ala Ser Pro Ser Ser His Ser Leu Ala Pro Pro
      565      570      575
Ser Gly Glu Arg Ser Arg Leu Ala Arg Gly Ser Thr Ile Arg Ser Thr
      580      585      590
Phe His Gly Gly Gln Val Arg Asp Arg Arg Ala Gly Gly Gly Gly
      595      600      605
Gly Gly Val Gln Asn Gly Pro Pro Ala Ser Pro Thr Leu Ala His Glu
      610      615      620
Ala Ala Pro Leu Pro Ala Gly Arg Pro Arg Pro Thr Thr Asn Leu Phe
625      630      635      640
Thr Lys Leu Thr Ser Lys Leu Thr Arg Ser Cys His Leu Pro Trp Asp
      645      650      655
Gln Thr Glu Thr Ala Pro Arg Leu Leu Arg Phe Pro Trp Ser Val Lys
      660      665      670
Leu Thr Ser Ser Arg Pro Pro Glu Ala Leu Met Ala Ala Leu Arg Gln
      675      680      685
Ala Thr Ala Ala Ala Arg Cys Arg Cys Arg Gln Pro Gln Pro Phe Leu
690      695      700
Leu Ala Cys Leu His Gly Gly Ala Gly Gly Pro Glu Pro Leu Ser His
705      710      715      720
Phe Glu Val Glu Val Cys Gln Leu Pro Arg Pro Gly Leu Arg Gly Val
      725      730      735
Leu Phe Arg Arg Val Ala Gly Thr Ala Leu Ala Phe Arg Thr Leu Val
740      745      750
Thr Arg Ile Ser Asn Asp Leu Glu Leu
      755      760

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<210> 43
 <211> 3234
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (3234)
 <223> MOOSE03372

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<400> 43
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Met Gly Arg Pro Gly Tyr Gly Ser Arg Ser His His Thr Pro Thr Ala
  1             5             10             15

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71/155

tct	ccg	gcc	agc	tgt	gca	aaa	agg	aac	gcg	tcc	tcc	ctg	ggc	cca	cgg	96
Ser	Pro	Ala	Ser	Cys	Ala	Lys	Arg	Asn	Ala	Ser	Ser	Leu	Gly	Pro	Arg	
			20					25					30			
ctg	ggt	ggc	cac	aca	gag	caa	gac	tcc	gtc	tca	gga	aaa	aga	aaa	aaa	144
Leu	Gly	Gly	His	Thr	Glu	Gln	Asp	Ser	Val	Ser	Gly	Lys	Arg	Lys	Lys	
		35					40					45				
aga	aaa	aag	aaa	cgg	agg	ccc	agg	ctg	atg	ata	tca	ccg	cca	ggg	gtg	192
Arg	Lys	Lys	Lys	Arg	Arg	Pro	Arg	Leu	Met	Ile	Ser	Pro	Pro	Gly	Val	
	50					55					60					
ccc	agc	agg	gac	agt	cgg	agc	agg	gct	gtg	agc	cgg	ggt	cag	ggc	cag	240
Pro	Ser	Arg	Asp	Ser	Arg	Ser	Arg	Ala	Val	Ser	Arg	Gly	Gln	Gly	Gln	
	65				70					75					80	
cag	aag	ccc	ctc	cgg	gtg	ggt	ttt	tac	gac	atc	gag	cgg	acc	ctg	ggc	288
Gln	Lys	Pro	Leu	Arg	Val	Gly	Phe	Tyr	Asp	Ile	Glu	Arg	Thr	Leu	Gly	
				85					90					95		
aaa	ggc	aac	ttc	gcg	gtg	gtg	aag	ctg	gcg	cgg	cat	cga	gtc	acc	aaa	336
Lys	Gly	Asn	Phe	Ala	Val	Val	Lys	Leu	Ala	Arg	His	Arg	Val	Thr	Lys	
			100					105					110			
acg	cag	gtt	gca	ata	aaa	ata	att	gat	aaa	aca	cga	tta	gat	tca	agc	384
Thr	Gln	Val	Ala	Ile	Lys	Ile	Ile	Asp	Lys	Thr	Arg	Leu	Asp	Ser	Ser	
		115					120					125				
aat	ttg	gag	aaa	atc	tat	cgt	gag	gtt	cag	ctg	atg	aag	ctt	ctg	aac	432
Asn	Leu	Glu	Lys	Ile	Tyr	Arg	Glu	Val	Gln	Leu	Met	Lys	Leu	Leu	Asn	
	130					135					140					
cat	cca	cac	atc	ata	aag	ctt	tac	cag	gtt	atg	gaa	aca	aag	gac	atg	480
His	Pro	His	Ile	Ile	Lys	Leu	Tyr	Gln	Val	Met	Glu	Thr	Lys	Asp	Met	
					150					155					160	
ctt	tac	atc	gtc	act	gaa	ttt	gct	aaa	aat	gga	gaa	atg	ttt	gat	tat	528
Leu	Tyr	Ile	Val	Thr	Glu	Phe	Ala	Lys	Asn	Gly	Glu	Met	Phe	Asp	Tyr	
				165					170					175		
ttg	act	tcc	aac	ggg	cac	ctg	agt	gag	aac	gag	gcg	cgg	aag	aag	ttc	576
Leu	Thr	Ser	Asn	Gly	His	Leu	Ser	Glu	Asn	Glu	Ala	Arg	Lys	Lys	Phe	
			180					185					190			
tgg	caa	atc	ctg	tcg	gcc	gtg	gag	tac	tgt	cac	gac	cat	cac	atc	gtc	624
Trp	Gln	Ile	Leu	Ser	Ala	Val	Glu	Tyr	Cys	His	Asp	His	His	Ile	Val	
		195					200					205				
cac	cgg	gac	ctc	aag	acc	gag	aac	ctc	ctg	ctg	gat	ggc	aac	atg	gac	672
His	Arg	Asp	Leu	Lys	Thr	Glu	Asn	Leu	Leu	Leu	Asp	Gly	Asn	Met	Asp	
	210					215					220					
atc	aag	ctg	gca	ggc	acg	gag	gat	ttt	gga	ttt	ggg	aat	ttc	tac	aag	720
Ile	Lys	Leu	Ala	Gly	Thr	Glu	Asp	Phe	Gly	Phe	Gly	Asn	Phe	Tyr	Lys	
					230					235					240	
tca	gga	gag	cct	ctg	tcc	acg	tgg	tgt	ggg	agc	ccc	ccg	tat	gcc	gcc	768
Ser	Gly	Glu	Pro	Leu	Ser	Thr	Trp	Cys	Gly	Ser	Pro	Pro	Tyr	Ala	Ala	
				245					250					255		

72/155

ccg gaa gtc ttt gag ggg aag gag tat gaa ggc ccc cag ctg gac atc	816
Pro Glu Val Phe Glu Gly Lys Glu Tyr Glu Gly Pro Gln Leu Asp Ile	
260 265 270	
tgg agc ctg ggc gtg gtg ctg tac gtc ctg gtc tgc ggt tct ctc ccc	864
Trp Ser Leu Gly Val Val Leu Tyr Val Leu Val Cys Gly Ser Leu Pro	
275 280 285	
ttc gat ggg cct aac ctg ccg acg ctg aga cag cgg gtg ctg gag ggc	912
Phe Asp Gly Pro Asn Leu Pro Thr Leu Arg Gln Arg Val Leu Glu Gly	
290 295 300	
cgc ttc cgc atc ccc ttc ttc atg tct caa gac tgt gag agc ctg atc	960
Arg Phe Arg Ile Pro Phe Phe Met Ser Gln Asp Cys Glu Ser Leu Ile	
305 310 315 320	
cgc cgc atg ctg gtg gtg gac ccc gcc agg cgc atc acc atc gcc cag	1008
Arg Arg Met Leu Val Val Asp Pro Ala Arg Arg Ile Thr Ile Ala Gln	
325 330 335	
atc cgg cag cac cgg tgg atg cgg gct gag ccc tgc ttg ccg gga ccc	1056
Ile Arg Gln His Arg Trp Met Arg Ala Glu Pro Cys Leu Pro Gly Pro	
340 345 350	
gcc tgc ccc gcc ttc tcc gca cac agc tac acc tcc aac ctg ggc gac	1104
Ala Cys Pro Ala Phe Ser Ala His Ser Tyr Thr Ser Asn Leu Gly Asp	
355 360 365	
tac gat gag cag gcg ctg ggt atc atg cag acc ctg ggc gtg gac cgg	1152
Tyr Asp Glu Gln Ala Leu Gly Ile Met Gln Thr Leu Gly Val Asp Arg	
370 375 380	
cag agg acg gtg gag tca ctg caa aac agc agc tat aac cac ttt gct	1200
Gln Arg Thr Val Glu Ser Leu Gln Asn Ser Ser Tyr Asn His Phe Ala	
385 390 395 400	
gcc att tat tac ctc ctc ctt gag cgg ctc aag gag tat cgg aat gcc	1248
Ala Ile Tyr Tyr Leu Leu Leu Glu Arg Leu Lys Glu Tyr Arg Asn Ala	
405 410 415	
cag tgc gcc cgc ccc ggg cct gcc agg cag ccg cgg cct cgg agc tcg	1296
Gln Cys Ala Arg Pro Gly Pro Ala Arg Gln Pro Arg Pro Arg Ser Ser	
420 425 430	
gac ctc agt ggt ttg gag gtg agg ggg agg agt ctc ctc cca ggc ccc	1344
Asp Leu Ser Gly Leu Glu Val Arg Gly Arg Ser Leu Leu Pro Gly Pro	
435 440 445	
agg ctc cct ccc ctg tca ggc acc ggc ttg gag ggc gga ctg gcc tct	1392
Arg Leu Pro Pro Leu Ser Gly Thr Gly Leu Glu Gly Gly Leu Ala Ser	
450 455 460	
cgg ggt ggg ggt ggg gag aga ggg gat gcc cca gcc aga ggg agg tcc	1440
Arg Gly Gly Gly Gly Glu Arg Gly Asp Ala Pro Ala Arg Gly Arg Ser	
465 470 475 480	
ctg ggc cca gcc tgg agg gag ccg agg caa gat cca cct aat tgt gat	1488
Leu Gly Pro Ala Trp Arg Glu Pro Arg Gln Asp Pro Pro Asn Cys Asp	
485 490 495	

73/155

gga atg aat ttc ggc agc cac agg aaa cta aga agc cca aac acg ccg	1536
Gly Met Asn Phe Gly Ser His Arg Lys Leu Arg Ser Pro Asn Thr Pro	
500 505 510	
gtt cct atc cgt gaa gga caa aag acc cac gcg ttg agt cac cag ggc	1584
Val Pro Ile Arg Glu Gly Gln Lys Thr His Ala Leu Ser His Gln Gly	
515 520 525	
tat cag gga aga gcc tgg gcc ggg gtc cta gcc cca gag ccc aga atc	1632
Tyr Gln Gly Arg Ala Trp Ala Gly Val Leu Ala Pro Glu Pro Arg Ile	
530 535 540	
ccc gct tcc agt tct cag ctg ccc cgt gag cgg gct gtc agc aac tcc	1680
Pro Ala Ser Ser Ser Gln Leu Pro Arg Glu Arg Ala Val Ser Asn Ser	
545 550 555 560	
cag cag cca ggc ctg tgg gct gag atg gtg gcg gtt tcc tgc cct gcc	1728
Gln Gln Pro Gly Leu Trp Ala Glu Met Val Ala Val Ser Cys Pro Ala	
565 570 575	
tct cct ccc ctg cgg ggt cag ggg gct cct ctg ctg acc ttg tac tta	1776
Ser Pro Pro Leu Arg Gly Gln Gly Ala Pro Leu Leu Thr Leu Tyr Leu	
580 585 590	
gaa acg aca cag ccc cat ggg ctg tgg gca tcc tcc agc cgg tgt ccc	1824
Glu Thr Thr Gln Pro His Gly Leu Trp Ala Ser Ser Ser Arg Cys Pro	
595 600 605	
atc tgc cct gca agc agt gcc tgg gct cag agc agc cca cag gac act	1872
Ile Cys Pro Ala Ser Ser Ser Ala Trp Ala Gln Ser Ser Pro Gln Asp Thr	
610 615 620	
gtc caa gat gcg cag acc ccg agg gcc aga ggg acc ggc tct gca gga	1920
Val Gln Asp Ala Gln Thr Pro Arg Ala Arg Gly Thr Gly Ser Ala Gly	
625 630 635 640	
atc cca cct cct ggg ccc act ccg cac aga gtg ttc tgc agg gcc tgg	1968
Ile Pro Pro Pro Gly Pro Thr Pro His Arg Val Phe Cys Arg Ala Trp	
645 650 655	
gag aac cag gca cct ggc cag gac agc ctg tgg gtg ggc agc cgt gtg	2016
Glu Asn Gln Ala Pro Gly Gln Asp Ser Leu Trp Val Gly Ser Arg Val	
660 665 670	
cac aga tac aca cac acg tca ggg aca gac aca cac aca cca ggg aca	2064
His Arg Tyr Thr His Thr Ser Gly Thr Asp Thr His Thr Pro Gly Thr	
675 680 685	
cac acc aca cac acc agg gac gca cac cac aca cac cag gga cac cca	2112
His Thr Thr His Thr Arg Asp Ala His His Thr His Gln Gly His Pro	
690 695 700	
cac aca cca cgg acg cac acc aca cac acc agg gac acc cac aca cac	2160
His Thr Pro Arg Thr His Thr Thr His Thr Arg Asp Thr His Thr His	
705 710 715 720	
cag gga cgc aca cca cac aca cca ggg acc cct gca cac acc agg gac	2208
Gln Gly Arg Thr Pro His Thr Pro Gly Thr Pro Ala His Thr Arg Asp	
725 730 735	

74/155

aca	cac	aca	cac	acc	ggg	gat	gca	cac	cac	aca	cac	acc	agg	gat	gca	2256
Thr	His	Thr	His	Thr	Gly	Asp	Ala	His	His	Thr	His	Thr	Arg	Asp	Ala	
			740					745					750			
tac	cac	aca	cac	cag	gga	ccc	aca	cac	aca	cca	ggg	acc	cac	aca	cac	2304
Tyr	His	Thr	His	Gln	Gly	Pro	Thr	His	Thr	Pro	Gly	Thr	His	Thr	His	
		755					760					765				
tcc	agg	gac	gca	cac	cac	aca	cac	cag	gga	ccc	ccg	caa	aca	cac	aca	2352
Ser	Arg	Asp	Ala	His	His	Thr	His	Gln	Gly	Pro	Pro	Gln	Thr	His	Thr	
	770					775					780					
cca	ggg	aca	cac	aca	cac	cag	gga	cac	aca	cac	cac	aca	cac	acc	agg	2400
Pro	Gly	Thr	His	Thr	His	Gln	Gly	His	Thr	His	His	Thr	His	Thr	Arg	
785					790					795					800	
gac	aca	cac	cac	aca	cac	cag	gga	cac	aca	cca	ggg	aca	gac	aca	caa	2448
Asp	Thr	His	His	Thr	His	Gln	Gly	His	Thr	Pro	Gly	Thr	Asp	Thr	Gln	
				805					810					815		
ggg	atg	cac	aca	cac	cag	gga	cgc	aca	gca	cac	aca	cca	ggg	acc	cat	2496
Gly	Met	His	Thr	His	Gln	Gly	Arg	Thr	Ala	His	Thr	Pro	Gly	Thr	His	
			820					825						830		
aca	cac	acc	agg	gat	gca	cac	aca	tca	ggg	aca	cac	aaa	cac	cag	gga	2544
Thr	His	Thr	Arg	Asp	Ala	His	Thr	Ser	Gly	Thr	His	Lys	His	Gln	Gly	
		835					840					845				
cgc	aca	cca	cac	aca	cca	ggg	aca	cac	acc	aca	cac	aca	cac	acc	atg	2592
Arg	Thr	Pro	His	Thr	Pro		Thr	His	Thr	Thr	His	Thr	His	Thr	Met	
	850					855						860				
gac	aca	cac	acc	act	ggg	aca	cgt	tgt	gaa	cac	acc	atg	gac	aca	cag	2640
Asp	Thr	His	Thr	Thr	Gly	Thr	Arg	Cys	Glu	His	Thr	Met	Asp	Thr	Gln	
865					870					875					880	
aga	aac	aca	cac	aac	atg	ggg	aca	cac	aac	aca	cac	cac	aaa	gac	ata	2688
Arg	Asn	Thr	His	Asn	Met	Gly	Thr	His	Asn	Thr	His	His	Lys	Asp	Ile	
				885					890					895		
acc	tcc	cca	cac	act	cac	ata	cat	aac	aca	cat	acc	aga	gac	aca	tgg	2736
Thr	Ser	Pro	His	Thr	His	Ile	His	Asn	Thr	His	Thr	Arg	Asp	Thr	Trp	
			900					905					910			
tta	cac	aca	gca	cac	act	ccc	tca	tca	gac	acc	cac	aca	cca	tct	cac	2784
Leu	His	Thr	Ala	His	Thr	Pro	Ser	Ser	Asp	Thr	His	Thr	Pro	Ser	His	
		915					920					925				
aca	cac	cac	aca	ccc	atc	aga	cac	cca	cac	atc	atc	tca	cac	acc	aca	2832
Thr	His	His	Thr	Pro	Ile	Arg	His	Pro	His	Ile	Ile	Ser	His	Thr	Thr	
		930				935					940					
cac	tca	cca	gac	acc	cac	aca	tca	tct	cac	aca	cac	cac	aca	ccc	atc	2880
His	Ser	Pro	Asp	Thr	His	Thr	Ser	Ser	His	Thr	His	His	Thr	Pro	Ile	
945					950					955					960	
aga	cac	cca	aca	tca	tct	cac	aca	cac	tac	aca	ctc	acc	aga	cac	cca	2928
Arg	His	Pro	Thr	Ser	Ser	His	Thr	His	Tyr	Thr	Leu	Thr	Arg	His	Pro	
				965					970					975		

75/155

cac atc atc tcg cac aca cca cac acc cat cag aca ccc aac atc atc 2976
 His Ile Ile Ser His Thr Pro His Thr His Gln Thr Pro Asn Ile Ile
 980 985 990

tca cag cag tca tat gca caa tta gag ggg gct tct cct agc ctg tgt 3024
 Ser Gln Gln Ser Tyr Ala Gln Leu Glu Gly Ala Ser Pro Ser Leu Cys
 995 1000 1005

tct cct cgg cat ccc tgg tgg ctt ggg gct ggg gag gga cac cca gct 3072
 Ser Pro Arg His Pro Trp Trp Leu Gly Ala Gly Glu Gly His Pro Ala
 1010 1015 1020

cct ccc gac cga cgt cta tgg ctt ctg gtg ctc cac tct cct ctc gga 3120
 Pro Pro Asp Arg Arg Leu Trp Leu Leu Val Leu His Ser Pro Leu Gly
 1025 1030 1035 1040

cag cag caa aca ttt aag atg gac ata gca gaa aga agg gag ccg gcc 3168
 Gln Gln Gln Thr Phe Lys Met Asp Ile Ala Glu Arg Arg Glu Pro Ala
 1045 1050 1055

atg tgc tcc cag caa aac cca aat gcc cgg ttc cct ctc tgc tcc tct 3216
 Met Cys Ser Gln Gln Asn Pro Asn Ala Arg Phe Pro Leu Cys Ser Ser
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ctc gct cct ctc cca ctc 3234
 Leu Ala Pro Leu Pro Leu
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 35 40 45
 Arg Lys Lys Lys Arg Arg Pro Arg Leu Met Ile Ser Pro Pro Gly Val
 50 55 60
 Pro Ser Arg Asp Ser Arg Ser Arg Ala Val Ser Arg Gly Gln Gly Gln
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 Gln Lys Pro Leu Arg Val Gly Phe Tyr Asp Ile Glu Arg Thr Leu Gly
 85 90 95
 Lys Gly Asn Phe Ala Val Val Lys Leu Ala Arg His Arg Val Thr Lys
 100 105 110
 Thr Gln Val Ala Ile Lys Ile Ile Asp Lys Thr Arg Leu Asp Ser Ser
 115 120 125
 Asn Leu Glu Lys Ile Tyr Arg Glu Val Gln Leu Met Lys Leu Leu Asn
 130 135 140
 His Pro His Ile Ile Lys Leu Tyr Gln Val Met Glu Thr Lys Asp Met
 145 150 155 160
 Leu Tyr Ile Val Thr Glu Phe Ala Lys Asn Gly Glu Met Phe Asp Tyr
 165 170 175
 Leu Thr Ser Asn Gly His Leu Ser Glu Asn Glu Ala Arg Lys Lys Phe
 180 185 190
 Trp Gln Ile Leu Ser Ala Val Glu Tyr Cys His Asp His His Ile Val
 195 200 205

76/155

His	Arg	Asp	Leu	Lys	Thr	Glu	Asn	Leu	Leu	Leu	Asp	Gly	Asn	Met	Asp
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Ile	Lys	Leu	Ala	Gly	Thr	Glu	Asp	Phe	Gly	Phe	Gly	Asn	Phe	Tyr	Lys
225					230					235					240
Ser	Gly	Glu	Pro	Leu	Ser	Thr	Trp	Cys	Gly	Ser	Pro	Pro	Tyr	Ala	Ala
				245					250					255	
Pro	Glu	Val	Phe	Glu	Gly	Lys	Glu	Tyr	Glu	Gly	Pro	Gln	Leu	Asp	Ile
			260					265					270		
Trp	Ser	Leu	Gly	Val	Val	Leu	Tyr	Val	Leu	Val	Cys	Gly	Ser	Leu	Pro
	275						280					285			
Phe	Asp	Gly	Pro	Asn	Leu	Pro	Thr	Leu	Arg	Gln	Arg	Val	Leu	Glu	Gly
	290					295					300				
Arg	Phe	Arg	Ile	Pro	Phe	Met	Ser	Gln	Asp	Cys	Glu	Ser	Leu	Ile	
305					310					315					320
Arg	Arg	Met	Leu	Val	Val	Asp	Pro	Ala	Arg	Arg	Ile	Thr	Ile	Ala	Gln
				325					330					335	
Ile	Arg	Gln	His	Arg	Trp	Met	Arg	Ala	Glu	Pro	Cys	Leu	Pro	Gly	Pro
			340					345					350		
Ala	Cys	Pro	Ala	Phe	Ser	Ala	His	Ser	Tyr	Thr	Ser	Asn	Leu	Gly	Asp
		355					360					365			
Tyr	Asp	Glu	Gln	Ala	Leu	Gly	Ile	Met	Gln	Thr	Leu	Gly	Val	Asp	Arg
	370					375					380				
Gln	Arg	Thr	Val	Glu	Ser	Leu	Gln	Asn	Ser	Ser	Tyr	Asn	His	Phe	Ala
385					390					395					400
Ala	Ile	Tyr	Tyr	Leu	Leu	Glu	Arg	Leu	Lys	Glu	Tyr	Arg	Asn	Ala	
				405				410						415	
Gln	Cys	Ala	Arg	Pro	Gly	Pro	Ala	Arg	Gln	Pro	Arg	Pro	Arg	Ser	Ser
			420					425					430		
Asp	Leu	Ser	Gly	Leu	Glu	Val	Arg	Gly	Arg	Ser	Leu	Leu	Pro	Gly	Pro
	435						440					445			
Arg	Leu	Pro	Pro	Leu	Ser	Gly	Thr	Gly	Leu	Glu	Gly	Gly	Leu	Ala	Ser
	450					455					460				
Arg	Gly	Gly	Gly	Gly	Glu	Arg	Gly	Asp	Ala	Pro	Ala	Arg	Gly	Arg	Ser
465					470					475					480
Leu	Gly	Pro	Ala	Trp	Arg	Glu	Pro	Arg	Gln	Asp	Pro	Pro	Asn	Cys	Asp
				485					490					495	
Gly	Met	Asn	Phe	Gly	Ser	His	Arg	Lys	Leu	Arg	Ser	Pro	Asn	Thr	Pro
			500					505					510		
Val	Pro	Ile	Arg	Glu	Gly	Gln	Lys	Thr	His	Ala	Leu	Ser	His	Gln	Gly
		515					520					525			
Tyr	Gln	Gly	Arg	Ala	Trp	Ala	Gly	Val	Leu	Ala	Pro	Glu	Pro	Arg	Ile
	530					535					540				
Pro	Ala	Ser	Ser	Ser	Gln	Leu	Pro	Arg	Glu	Arg	Ala	Val	Ser	Asn	Ser
545					550					555					560
Gln	Gln	Pro	Gly	Leu	Trp	Ala	Glu	Met	Val	Ala	Val	Ser	Cys	Pro	Ala
				565					570					575	
Ser	Pro	Pro	Leu	Arg	Gly	Gln	Gly	Ala	Pro	Leu	Leu	Thr	Leu	Tyr	Leu
			580					585					590		
Glu	Thr	Thr	Gln	Pro	His	Gly	Leu	Trp	Ala	Ser	Ser	Ser	Arg	Cys	Pro
		595					600					605			
Ile	Cys	Pro	Ala	Ser	Ser	Ala	Trp	Ala	Gln	Ser	Ser	Pro	Gln	Asp	Thr
	610					615					620				
Val	Gln	Asp	Ala	Gln	Thr	Pro	Arg	Ala	Arg	Gly	Thr	Gly	Ser	Ala	Gly
625					630					635					640
Ile	Pro	Pro	Pro	Gly	Pro	Thr	Pro	His	Arg	Val	Phe	Cys	Arg	Ala	Trp
				645					650					655	
Glu	Asn	Gln	Ala	Pro	Gly	Gln	Asp	Ser	Leu	Trp	Val	Gly	Ser	Arg	Val
			660					665					670		
His	Arg	Tyr	Thr	His	Thr	Ser	Gly	Thr	Asp	Thr	His	Thr	Pro	Gly	Thr
		675					680					685			
His	Thr	Thr	His	Thr	Arg	Asp	Ala	His	His	Thr	His	Gln	Gly	His	Pro
	690					695						700			

77/155

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His Thr Pro Arg Thr His Thr Thr His Thr Arg Asp Thr His Thr His
705          710          715          720
Gln Gly Arg Thr Pro His Thr Pro Gly Thr Pro Ala His Thr Arg Asp
          725          730          735
Thr His Thr His Thr Gly Asp Ala His His Thr His Thr Arg Asp Ala
          740          745          750
Tyr His Thr His Gln Gly Pro Thr His Thr Pro Gly Thr His Thr His
          755          760          765
Ser Arg Asp Ala His His Thr His Gln Gly Pro Pro Gln Thr His Thr
          770          775          780
Pro Gly Thr His Thr His Gln Gly His Thr His His Thr His Thr Arg
785          790          795          800
Asp Thr His His Thr His Gln Gly His Thr Pro Gly Thr Asp Thr Gln
          805          810          815
Gly Met His Thr His Gln Gly Arg Thr Ala His Thr Pro Gly Thr His
          820          825          830
Thr His Thr Arg Asp Ala His Thr Ser Gly Thr His Lys His Gln Gly
          835          840          845
Arg Thr Pro His Thr Pro Gly Thr His Thr Thr His Thr His Thr Met
          850          855          860
Asp Thr His Thr Thr Gly Thr Arg Cys Glu His Thr Met Asp Thr Gln
865          870          875          880
Arg Asn Thr His Asn Met Gly Thr His Asn Thr His His Lys Asp Ile
          885          890          895
Thr Ser Pro His Thr His Ile His Asn Thr His Thr Arg Asp Thr Trp
          900          905          910
Leu His Thr Ala His Thr Pro Ser Ser Asp Thr His Thr Pro Ser His
          915          920          925
Thr His His Thr Pro Ile Arg His Pro His Ile Ile Ser His Thr Thr
          930          935          940
His Ser Pro Asp Thr His Thr Ser Ser His Thr His His Thr Pro Ile
945          950          955          960
Arg His Pro Thr Ser Ser His Thr His Tyr Thr Leu Thr Arg His Pro
          965          970          975
His Ile Ile Ser His Thr Pro His Thr His Gln Thr Pro Asn Ile Ile
          980          985          990
Ser Gln Gln Ser Tyr Ala Gln Leu Glu Gly Ala Ser Pro Ser Leu Cys
          995          1000          1005
Ser Pro Arg His Pro Trp Trp Leu Gly Ala Gly Glu Gly His Pro Ala
1010          1015          1020
Pro Pro Asp Arg Arg Leu Trp Leu Leu Val Leu His Ser Pro Leu Gly
1025          1030          1035          1040
Gln Gln Gln Thr Phe Lys Met Asp Ile Ala Glu Arg Arg Glu Pro Ala
          1045          1050          1055
Met Cys Ser Gln Gln Asn Pro Asn Ala Arg Phe Pro Leu Cys Ser Ser
          1060          1065          1070
Leu Ala Pro Leu Pro Leu
          1075

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<400> 45

78/155

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gtt act aca gta ccc cat gtg ttt tca aaa ctg tta gaa atg ctg agt	96
Val Thr Thr Val Pro His Val Phe Ser Lys Leu Leu Glu Met Leu Ser	
20 25 30	
gtt tcc agt tcc act cac ttc acc agg atg cgt cgc cgt ttg atg gct	144
Val Ser Ser Ser Thr His Phe Thr Arg Met Arg Arg Arg Leu Met Ala	
35 40 45	
att gca gat gag gtg gaa att gcc gaa gcc atc cag ttg ggc gta gaa	192
Ile Ala Asp Glu Val Glu Ile Ala Glu Ala Ile Gln Leu Gly Val Glu	
50 55 60	
gac act ttg gat ggt caa cag gac agc ttc ttg cag gca tct gtt ccc	240
Asp Thr Leu Asp Gly Gln Gln Asp Ser Phe Leu Gln Ala Ser Val Pro	
65 70 75 80	
aac aac tat ctg gaa acc aca gag aac agt tcc cct gag tgc aca atc	288
Asn Asn Tyr Leu Glu Thr Thr Glu Asn Ser Ser Pro Glu Cys Thr Ile	
85 90 95	
cat tta gag aaa act gga aaa gga tta tgt gct aca aaa ttg agt gcc	336
His Leu Glu Lys Thr Gly Lys Gly Leu Cys Ala Thr Lys Leu Ser Ala	
100 105 110	
agt tca gag gac att tct gag aga ctg gcc agc att tca gta gga cct	384
Ser Ser Glu Asp Ile Ser Glu Arg Leu Ala Ser Ile Ser Val Gly Pro	
115 120 125	
tct agt tca aca aca aca aca aca aca gag caa cca aag cca atg	432
Ser Ser Ser Thr Thr Thr Thr Thr Thr Thr Glu Gln Pro Lys Pro Met	
130 135 140	
gtt caa aca aaa ggc aga ccc cac agt cag tgt ttg aac tcc tct cct	480
Val Gln Thr Lys Gly Arg Pro His Ser Gln Cys Leu Asn Ser Ser Pro	
145 150 155 160	
tta tct cat cat tcc caa tta atg ttt cca gcc ttg tca acc cct tct	528
Leu Ser His His Ser Gln Leu Met Phe Pro Ala Leu Ser Thr Pro Ser	
165 170 175	
tct tct acc cca tct gta cca gct ggc act gca aca gat gtc tct aag	576
Ser Ser Thr Pro Ser Val Pro Ala Gly Thr Ala Thr Asp Val Ser Lys	
180 185 190	
cat aga ctt cag gga ttc att ccc tgc aga ata cct tct gca tct cct	624
His Arg Leu Gln Gly Phe Ile Pro Cys Arg Ile Pro Ser Ala Ser Pro	
195 200 205	
caa aca cag cgc aag ttt tct cta caa ttc cac aga aac tgt cct gaa	672
Gln Thr Gln Arg Lys Phe Ser Leu Gln Phe His Arg Asn Cys Pro Glu	
210 215 220	
aac aaa gac tca gat aaa ctt tcc cca gtc ttt act cag tca aga ccc	720
Asn Lys Asp Ser Asp Lys Leu Ser Pro Val Phe Thr Gln Ser Arg Pro	
225 230 235 240	

79/155

ttg	ccc	tcc	agt	aac	ata	cac	agg	cca	aag	cca	tct	cga	cct	acc	cca	768
Leu	Pro	Ser	Ser	Asn	Ile	His	Arg	Pro	Lys	Pro	Ser	Arg	Pro	Thr	Pro	
				245					250					255		
ggt	aat	aca	agt	aaa	cag	gga	gat	ccc	tca	aaa	aat	agc	atg	aca	ctt	816
Gly	Asn	Thr	Ser	Lys	Gln	Gly	Asp	Pro	Ser	Lys	Asn	Ser	Met	Thr	Leu	
			260					265					270			
gat	ctg	aac	agt	agt	tcc	aaa	tgt	gat	gac	agc	ttt	ggc	tgt	agc	agc	864
Asp	Leu	Asn	Ser	Ser	Ser	Lys	Cys	Asp	Asp	Ser	Phe	Gly	Cys	Ser	Ser	
		275					280					285				
aat	agt	agt	aat	gct	gtt	ata	ccc	agt	gac	gag	aca	gtg	ttc	acc	cca	912
Asn	Ser	Ser	Asn	Ala	Val	Ile	Pro	Ser	Asp	Glu	Thr	Val	Phe	Thr	Pro	
	290					295					300					
gta	gag	gag	aaa	tgc	aga	tta	gat	gtc	aat	aca	gag	ctc	aac	tcc	agt	960
Val	Glu	Glu	Lys	Cys	Arg	Leu	Asp	Val	Asn	Thr	Glu	Leu	Asn	Ser	Ser	
305					310					315					320	
att	gag	gac	ctt	ctt	gaa	gca	tct	atg	cct	tca	agt	gat	aca	aca	gta	1008
Ile	Glu	Asp	Leu	Leu	Glu	Ala	Ser	Met	Pro	Ser	Ser	Asp	Thr	Thr	Val	
			325						330					335		
act	ttt	aag	tca	gaa	gtt	gct	gtc	ctg	tct	cct	gaa	aag	gct	gaa	aat	1056
Thr	Phe	Lys	Ser	Glu	Val	Ala	Val	Leu	Ser	Pro	Glu	Lys	Ala	Glu	Asn	
		340						345					350			
gat	gat	acc	tac	aaa	gat	gat	gtg	aat	cat	aat	caa	aag	tgc	aaa	gag	1104
Asp	Asp	Thr	Tyr	Lys	Asp	Asp	Val	Asn	His	Asn	Gln	Lys	Cys	Lys	Glu	
		355					360					365				
aag	atg	gaa	gct	gaa	gaa	gaa	gaa	gct	tta	gca	att	gcc	atg	gca	atg	1152
Lys	Met	Glu	Ala	Glu	Glu	Glu	Glu	Ala	Leu	Ala	Ile	Ala	Met	Ala	Met	
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tca	gcg	tct	cag	gat	gcc	ctc	ccc	ata	gtt	cct	cag	ctg	cag	gtt	gaa	1200
Ser	Ala	Ser	Gln	Asp	Ala	Leu	Pro	Ile	Val	Pro	Gln	Leu	Gln	Val	Glu	
385					390					395					400	
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Asn	Gly	Glu	Asp	Ile	Ile	Ile	Ile	Gln	Gln	Asp	Thr	Pro	Glu	Thr	Leu	
			405					410						415		
cca	gga	cat	acc	aaa	gca	aaa	caa	ccg	tat	aga	gaa	gac	act	gaa	tgg	1296
Pro	Gly	His	Thr	Lys	Ala	Lys	Gln	Pro	Tyr	Arg	Glu	Asp	Thr	Glu	Trp	
			420					425					430			
ctg	aaa	ggt	caa	cag	ata	ggc	ctt	gga	gca	ttt	tct	tct	tgt	tat	cag	1344
Leu	Lys	Gly	Gln	Gln	Ile	Gly	Leu	Gly	Ala	Phe	Ser	Ser	Cys	Tyr	Gln	
		435					440					445				
gct	caa	gat	gtg	gga	act	gga	act	tta	atg	gct	gtt	aaa	cag	gtg	act	1392
Ala	Gln	Asp	Val	Gly	Thr	Gly	Thr	Leu	Met	Ala	Val	Lys	Gln	Val	Thr	
	450					455					460					
tat	gtc	aga	aac	aca	tct	tct	gag	caa	gaa	gaa	gta	gta	gaa	gca	cta	1440
Tyr	Val	Arg	Asn	Thr	Ser	Ser	Glu	Gln	Glu	Glu	Val	Val	Glu	Ala	Leu	
465					470				475						480	

80/155

aga gaa gag ata aga atg atg agc cat ctg aat cat cca aac atc att	1488
Arg Glu Glu Ile Arg Met Met Ser His Leu Asn His Pro Asn Ile Ile	
485 490 495	
agg atg ttg gga gcc acg tgt gag aag agc aat tac aat ctc ttc att	1536
Arg Met Leu Gly Ala Thr Cys Glu Lys Ser Asn Tyr Asn Leu Phe Ile	
500 505 510	
gaa tgg atg gca ggg gga tcg gtg gct cat ttg ctg agt aaa tat gga	1584
Glu Trp Met Ala Gly Gly Ser Val Ala His Leu Leu Ser Lys Tyr Gly	
515 520 525	
gcc ttc aaa gaa tca gta gtt att aac tac act gaa cag tta ctc cgt	1632
Ala Phe Lys Glu Ser Val Val Ile Asn Tyr Thr Glu Gln Leu Leu Arg	
530 535 540	
ggc ctt tcg tat ctc cat gaa aac caa atc att cac aga gat gtc aaa	1680
Gly Leu Ser Tyr Leu His Glu Asn Gln Ile Ile His Arg Asp Val Lys	
545 550 555 560	
ggg gcc aat ttg cta att gac agc act ggt cag aga cta aga att gca	1728
Gly Ala Asn Leu Leu Ile Asp Ser Thr Gly Gln Arg Leu Arg Ile Ala	
565 570 575	
gat ttt gga gct gca gcc agg ttg gca tca aaa gga act ggt gca gga	1776
Asp Phe Gly Ala Ala Arg Leu Ala Ser Lys Gly Thr Gly Ala Gly	
580 585 590	
gag ttt cag gga caa tta ctg ggg aca att gca ttt atg gca cct gag	1824
Glu Phe Gln Gly Gln Leu Leu Gly Thr Ile Ala Phe Met Ala Pro Glu	
595 600 605	
gta cta aga ggt caa cag tat gga agg agc tgt gat gta tgg agt gtt	1872
Val Leu Arg Gly Gln Gln Tyr Gly Arg Ser Cys Asp Val Trp Ser Val	
610 615 620	
ggc tgt gct att ata gaa atg gct tgt gca aaa cca cca tgg aat gca	1920
Gly Cys Ala Ile Ile Glu Met Ala Cys Ala Lys Pro Pro Trp Asn Ala	
625 630 635 640	
gaa aaa cac tcc aat cat ctt gct ttg ata ttt aag att gct agt gca	1968
Glu Lys His Ser Asn His Leu Ala Leu Ile Phe Lys Ile Ala Ser Ala	
645 650 655	
act act gct cca tcg atc cct tca cat ttg tct cct ggt tta cga gat	2016
Thr Thr Ala Pro Ser Ile Pro Ser His Leu Ser Pro Gly Leu Arg Asp	
660 665 670	
gtg gct ctt cgt tgt tta gaa ctt caa cct cag gac aga cct cca tca	2064
Val Ala Leu Arg Cys Leu Glu Leu Gln Pro Gln Asp Arg Pro Pro Ser	
675 680 685	
aga gag cta ctg aag cat cca gtc ttt cgt act aca tgg	2103
Arg Glu Leu Leu Lys His Pro Val Phe Arg Thr Thr Trp	
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81/155

<400> 46
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Val Ser Ser Ser Thr His Phe Thr Arg Met Arg Arg Arg Leu Met Ala
35 40 45
Ile Ala Asp Glu Val Glu Ile Ala Glu Ala Ile Gln Leu Gly Val Glu
50 55 60
Asp Thr Leu Asp Gly Gln Gln Asp Ser Phe Leu Gln Ala Ser Val Pro
65 70 75 80
Asn Asn Tyr Leu Glu Thr Thr Glu Asn Ser Ser Pro Glu Cys Thr Ile
85 90 95
His Leu Glu Lys Thr Gly Lys Gly Leu Cys Ala Thr Lys Leu Ser Ala
100 105 110
Ser Ser Glu Asp Ile Ser Glu Arg Leu Ala Ser Ile Ser Val Gly Pro
115 120 125
Ser Ser Ser Thr Thr Thr Thr Thr Thr Glu Gln Pro Lys Pro Met
130 135 140
Val Gln Thr Lys Gly Arg Pro His Ser Gln Cys Leu Asn Ser Ser Pro
145 150 155 160
Leu Ser His His Ser Gln Leu Met Phe Pro Ala Leu Ser Thr Pro Ser
165 170 175
Ser Ser Thr Pro Ser Val Pro Ala Gly Thr Ala Thr Asp Val Ser Lys
180 185 190
His Arg Leu Gln Gly Phe Ile Pro Cys Arg Ile Pro Ser Ala Ser Pro
195 200 205
Gln Thr Gln Arg Lys Phe Ser Leu Gln Phe His Arg Asn Cys Pro Glu
210 215 220
Asn Lys Asp Ser Asp Lys Leu Ser Pro Val Phe Thr Gln Ser Arg Pro
225 230 235 240
Leu Pro Ser Ser Asn Ile His Arg Pro Lys Pro Ser Arg Pro Thr Pro
245 250 255
Gly Asn Thr Ser Lys Gln Gly Asp Pro Ser Lys Asn Ser Met Thr Leu
260 265 270
Asp Leu Asn Ser Ser Ser Lys Cys Asp Asp Ser Phe Gly Cys Ser Ser
275 280 285
Asn Ser Ser Asn Ala Val Ile Pro Ser Asp Glu Thr Val Phe Thr Pro
290 295 300
Val Glu Glu Lys Cys Arg Leu Asp Val Asn Thr Glu Leu Asn Ser Ser
305 310 315 320
Ile Glu Asp Leu Leu Glu Ala Ser Met Pro Ser Ser Asp Thr Thr Val
325 330 335
Thr Phe Lys Ser Glu Val Ala Val Leu Ser Pro Glu Lys Ala Glu Asn
340 345 350
Asp Asp Thr Tyr Lys Asp Asp Val Asn His Asn Gln Lys Cys Lys Glu
355 360 365
Lys Met Glu Ala Glu Glu Glu Glu Ala Leu Ala Ile Ala Met Ala Met
370 375 380
Ser Ala Ser Gln Asp Ala Leu Pro Ile Val Pro Gln Leu Gln Val Glu
385 390 395 400
Asn Gly Glu Asp Ile Ile Ile Ile Gln Gln Asp Thr Pro Glu Thr Leu
405 410 415
Pro Gly His Thr Lys Ala Lys Gln Pro Tyr Arg Glu Asp Thr Glu Trp
420 425 430
Leu Lys Gly Gln Gln Ile Gly Leu Gly Ala Phe Ser Ser Cys Tyr Gln
435 440 445
Ala Gln Asp Val Gly Thr Gly Thr Leu Met Ala Val Lys Gln Val Thr
450 455 460
Tyr Val Arg Asn Thr Ser Ser Glu Gln Glu Glu Val Val Glu Ala Leu
465 470 475 480

82/155

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Arg Glu Glu Ile Arg Met Met Ser His Leu Asn His Pro Asn Ile Ile
      485      490      495
Arg Met Leu Gly Ala Thr Cys Glu Lys Ser Asn Tyr Asn Leu Phe Ile
      500      505      510
Glu Trp Met Ala Gly Gly Ser Val Ala His Leu Leu Ser Lys Tyr Gly
      515      520      525
Ala Phe Lys Glu Ser Val Val Ile Asn Tyr Thr Glu Gln Leu Leu Arg
      530      535      540
Gly Leu Ser Tyr Leu His Glu Asn Gln Ile Ile His Arg Asp Val Lys
545      550      555      560
Gly Ala Asn Leu Leu Ile Asp Ser Thr Gly Gln Arg Leu Arg Ile Ala
      565      570      575
Asp Phe Gly Ala Ala Arg Leu Ala Ser Lys Gly Thr Gly Ala Gly
      580      585      590
Glu Phe Gln Gly Gln Leu Leu Gly Thr Ile Ala Phe Met Ala Pro Glu
      595      600      605
Val Leu Arg Gly Gln Gln Tyr Gly Arg Ser Cys Asp Val Trp Ser Val
610      615      620
Gly Cys Ala Ile Ile Glu Met Ala Cys Ala Lys Pro Pro Trp Asn Ala
625      630      635      640
Glu Lys His Ser Asn His Leu Ala Leu Ile Phe Lys Ile Ala Ser Ala
      645      650      655
Thr Thr Ala Pro Ser Ile Pro Ser His Leu Ser Pro Gly Leu Arg Asp
      660      665      670
Val Ala Leu Arg Cys Leu Glu Leu Gln Pro Gln Asp Arg Pro Pro Ser
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Arg Glu Leu Leu Lys His Pro Val Phe Arg Thr Thr Trp
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 <213> Homo sapiens

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 <223> MOOSE03452

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agg gtg tac aag ggt cga aga aaa tac agt gct cag gtc gtg gcc ctg 96
Arg Val Tyr Lys Gly Arg Arg Lys Tyr Ser Ala Gln Val Val Ala Leu
      20      25      30

aag ttc atc cca aaa ttg ggg cgc tca gag aag gag ctg agg aat ttg 144
Lys Phe Ile Pro Lys Leu Gly Arg Ser Glu Lys Glu Leu Arg Asn Leu
      35      40      45

caa cga gag att gaa ata atg cgg ggt ctg cgg cat ccc aac att gtg 192
Gln Arg Glu Ile Glu Ile Met Arg Gly Leu Arg His Pro Asn Ile Val
      50      55      60

cat atg ctt gac agc ttt gaa act gat aaa gag gtg gtg gtg gtg aca 240
His Met Leu Asp Ser Phe Glu Thr Asp Lys Glu Val Val Val Val Thr
65      70      75      80

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83/155

gac tat gct gag gga gag ctc ttt cag atc cta gaa gat gac gga aaa	288
Asp Tyr Ala Glu Gly Glu Leu Phe Gln Ile Leu Glu Asp Asp Gly Lys	
85 90 95	
ctt cct gaa gac cag gtt cag gcc att gct gcc cag ttg gtg tca gcc	336
Leu Pro Glu Asp Gln Val Gln Ala Ile Ala Ala Gln Leu Val Ser Ala	
100 105 110	
ctg tac tat ctg cat tcc cac cgc atc cta cac cga gat atg aag cct	384
Leu Tyr Tyr Leu His Ser His Arg Ile Leu His Arg Asp Met Lys Pro	
115 120 125	
cag aac atc ctc ctc gcc aag ggt ggt ggc atc aag ctc tgt gac ttt	432
Gln Asn Ile Leu Leu Ala Lys Gly Gly Gly Ile Lys Leu Cys Asp Phe	
130 135 140	
gga ttt gcc cgg gct atg agc acc aat aca atg gtg ctg aca tcc atc	480
Gly Phe Ala Arg Ala Met Ser Thr Asn Thr Met Val Leu Thr Ser Ile	
145 150 155 160	
aaa ggc aca cca ctc tat atg tct cca gag ctg gtg gag gag cga cca	528
Lys Gly Thr Pro Leu Tyr Met Ser Pro Glu Leu Val Glu Glu Arg Pro	
165 170 175	
tac gac cac aca gcg gac ctc tgg tct gtt ggc tgc ata cta tat gaa	576
Tyr Asp His Thr Ala Asp Leu Trp Ser Val Gly Cys Ile Leu Tyr Glu	
180 185 190	
ctg gca gta ggc acc cct ccc ttc tat gct aca agc atc ttt cag ctg	624
Leu Ala Val Gly Thr Pro Pro Phe Tyr Ala Thr Ser Ile Phe Gln Leu	
195 200 205	
gtc agc ctc att ctc aag gac cct gtg cgc tgg ccc tca acc atc agt	672
Val Ser Leu Ile Leu Lys Asp Pro Val Arg Trp Pro Ser Thr Ile Ser	
210 215 220	
ccc tgc ttt aag aac ttc ctg cag gga ctg ctc acc aaa gac cca cgg	720
Pro Cys Phe Lys Asn Phe Leu Gln Gly Leu Leu Thr Lys Asp Pro Arg	
225 230 235 240	
cag cga ctg tcc tgg cca gac ctc tta tat cac ccc ttt att gct ggt	768
Gln Arg Leu Ser Trp Pro Asp Leu Leu Tyr His Pro Phe Ile Ala Gly	
245 250 255	
cat gtc acc ata ata act gag cca gca ggc cca gat ttg ggg acc cca	816
His Val Thr Ile Ile Thr Glu Pro Ala Gly Pro Asp Leu Gly Thr Pro	
260 265 270	
ttc acc agc cgc cta ccc cca gaa ctt cag gtc cta aag gac gaa cag	864
Phe Thr Ser Arg Leu Pro Pro Glu Leu Gln Val Leu Lys Asp Glu Gln	
275 280 285	
gcc cat cgg ttg gcc ccc aag ggt aat cag tct cgc atc ttg act cag	912
Ala His Arg Leu Ala Pro Lys Gly Asn Gln Ser Arg Ile Leu Thr Gln	
290 295 300	
gcc tat aaa cgc atg gct gag gag gcc atg cag aag gtt gca gtg agc	960
Ala Tyr Lys Arg Met Ala Glu Glu Ala Met Gln Lys Val Ala Val Ser	
305 310 315 320	

84/155

caa gat tac gcc act gaa ctc cag cct ggt gac aga gca aga ctc cgt	1008
Gln Asp Tyr Ala Thr 325 Glu Leu Gln Pro Gly 330 Asp Arg Ala Arg Leu Arg 335	
ctc aaa aaa aaa aaa aaa aaa aag caa tta aac tta tac cta aac ttt	1056
Leu Lys Lys Lys Lys Lys Lys Lys Gln 345 Leu Asn Leu Tyr 350 Leu Asn Phe 350	
tta gac tat cta gca cat aaa gca ata atg gat tct gaa gtt aag gct	1104
Leu Asp Tyr Leu Ala His Lys Ala 360 Ile Met Asp Ser 365 Glu Val Lys Ala 365	
tca tct aga tac aga ttt tca gca aat gac aac ttc cta ttc aca cat	1152
Ser Ser Arg Tyr Arg Phe Ser 375 Ala Asn Asp Asn 380 Phe Leu Phe Thr His 380	
tca ttt ctg cat ttg gtt atg ctg ggg gcg ggc gga tcg ctt gag cag	1200
Ser Phe Leu His Leu 390 Val Met Leu Gly Ala 395 Gly Gly Ser Leu Glu Gln 400	
gag ttc aag ttc gca gtg agc tat gat cac gtc gct gca ctc cag cct	1248
Glu Phe Lys Phe Ala 405 Val Ser Tyr Asp 410 His Val Ala Ala Leu Gln Pro 415	
ggg cga cag agc gag att ctg tct cta aaa aag aaa aca gtc cat agg	1296
Gly Arg Gln Ser 420 Glu Ile Leu Ser 425 Leu Lys Lys Lys Thr 430 Val His Arg 430	
gat aga aag aga gag tcc tgg atg ctc cga atg gag cct ttc aga gct	1344
Asp Arg Lys Arg Glu Ser Trp 440 Met Leu Arg Met Glu 445 Pro Phe Arg Ala 445	
tta acc acg gga cta cat ctc cca gaa ttc cgc tcg ccg gat ccc acc	1392
Leu Thr Thr Gly Leu His 455 Leu Pro Glu Phe Arg Ser 460 Pro Pro Asp Pro Thr 460	
gca ctg aag gga ctg cgc gtg cgc gag tca ggt gac gac ccg ccc cta	1440
Ala Leu Lys Gly Leu Arg 470 Val Arg Glu Ser 475 Gly Asp Asp Pro Pro Leu 480	
cag gcc cca gaa ccc ccg aga ttc ccc gcg ctt gcc tcc cgc cct ctt	1488
Gln Ala Pro Glu Pro 485 Pro Arg Phe Pro 490 Ala Leu Ala Ser Arg Pro Leu 495	
ctt cca gac tct cgg tct aaa agc cta aaa aag aaa ata aaa att aca	1536
Leu Pro Asp Ser Arg Ser Lys Ser 505 Leu Lys Lys Lys Ile 510 Lys Ile Thr 510	
tat aat tta cca ccg ttg tta att ttg gta ggt act ttt cca gtc gag	1584
Tyr Asn Leu Pro Pro Leu Leu 520 Ile Leu Val Gly Thr 525 Phe Pro Val Glu 525	
tgt gtg cat gtg aaa tca gct gtt gaa ata gtt ttg agt gag cca cca	1632
Cys Val His Val Lys Ser 535 Ala Val Glu Ile Val 540 Leu Ser Glu Pro Pro 540	
cac cag gtc tgt ttt tgt gtt ttc ttt tct ttt gag atg gag tct tgc	1680
His Gln Val Cys Phe 550 Cys Val Phe Phe Ser 555 Glu Met Glu Ser Cys 560	

85/155

tct gta cct cag ctg gaa tta cag aaa tca ccc gtc ttc tgc gtt gat	1728
Ser Val Pro Gln Leu Glu Leu Gln Lys Ser Pro Val Phe Cys Val Asp	
565 570 575	
cac gtt ggg agc agc aga tca gag ctg ttc cta ttc ggc cat ctt tct	1776
His Val Gly Ser Ser Arg Ser Glu Leu Phe Leu Phe Gly His Leu Ser	
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ttt ctt tct ttt ctt tcc	1794
Phe Leu Ser Phe Leu Ser	
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 <212> PRT
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20 25 30	
Lys Phe Ile Pro Lys Leu Gly Arg Ser Glu Lys Glu Leu Arg Asn Leu	
35 40 45	
Gln Arg Glu Ile Glu Ile Met Arg Gly Leu Arg His Pro Asn Ile Val	
50 55 60	
His Met Leu Asp Ser Phe Glu Thr Asp Lys Glu Val Val Val Val Thr	
65 70 75 80	
Asp Tyr Ala Glu Gly Glu Leu Phe Gln Ile Leu Glu Asp Asp Gly Lys	
85 90 95	
Leu Pro Glu Asp Gln Val Gln Ala Ile Ala Ala Gln Leu Val Ser Ala	
100 105 110	
Leu Tyr Tyr Leu His Ser His Arg Ile Leu His Arg Asp Met Lys Pro	
115 120 125	
Gln Asn Ile Leu Leu Ala Lys Gly Gly Gly Ile Lys Leu Cys Asp Phe	
130 135 140	
Gly Phe Ala Arg Ala Met Ser Thr Asn Thr Met Val Leu Thr Ser Ile	
145 150 155 160	
Lys Gly Thr Pro Leu Tyr Met Ser Pro Glu Leu Val Glu Glu Arg Pro	
165 170 175	
Tyr Asp His Thr Ala Asp Leu Trp Ser Val Gly Cys Ile Leu Tyr Glu	
180 185 190	
Leu Ala Val Gly Thr Pro Pro Phe Tyr Ala Thr Ser Ile Phe Gln Leu	
195 200 205	
Val Ser Leu Ile Leu Lys Asp Pro Val Arg Trp Pro Ser Thr Ile Ser	
210 215 220	
Pro Cys Phe Lys Asn Phe Leu Gln Gly Leu Leu Thr Lys Asp Pro Arg	
225 230 235 240	
Gln Arg Leu Ser Trp Pro Asp Leu Leu Tyr His Pro Phe Ile Ala Gly	
245 250 255	
His Val Thr Ile Ile Thr Glu Pro Ala Gly Pro Asp Leu Gly Thr Pro	
260 265 270	
Phe Thr Ser Arg Leu Pro Pro Glu Leu Gln Val Leu Lys Asp Glu Gln	
275 280 285	
Ala His Arg Leu Ala Pro Lys Gly Asn Gln Ser Arg Ile Leu Thr Gln	
290 295 300	
Ala Tyr Lys Arg Met Ala Glu Glu Ala Met Gln Lys Val Ala Val Ser	
305 310 315 320	
Gln Asp Tyr Ala Thr Glu Leu Gln Pro Gly Asp Arg Ala Arg Leu Arg	
325 330 335	

86/155

Leu Lys Lys Lys Lys Lys Lys Lys Gln Leu Asn Leu Tyr Leu Asn Phe
 340 345 350
 Leu Asp Tyr Leu Ala His Lys Ala Ile Met Asp Ser Glu Val Lys Ala
 355 360 365
 Ser Ser Arg Tyr Arg Phe Ser Ala Asn Asp Asn Phe Leu Phe Thr His
 370 375 380
 Ser Phe Leu His Leu Val Met Leu Gly Ala Gly Gly Ser Leu Glu Gln
 385 390 395 400
 Glu Phe Lys Phe Ala Val Ser Tyr Asp His Val Ala Ala Leu Gln Pro
 405 410 415
 Gly Arg Gln Ser Glu Ile Leu Ser Leu Lys Lys Lys Thr Val His Arg
 420 425 430
 Asp Arg Lys Arg Glu Ser Trp Met Leu Arg Met Glu Pro Phe Arg Ala
 435 440 445
 Leu Thr Thr Gly Leu His Leu Pro Glu Phe Arg Ser Pro Asp Pro Thr
 450 455 460
 Ala Leu Lys Gly Leu Arg Val Arg Glu Ser Gly Asp Asp Pro Pro Leu
 465 470 475 480
 Gln Ala Pro Glu Pro Arg Phe Pro Ala Leu Ala Ser Arg Pro Leu
 485 490 495
 Leu Pro Asp Ser Arg Ser Lys Ser Leu Lys Lys Lys Ile Lys Ile Thr
 500 505 510
 Tyr Asn Leu Pro Pro Leu Leu Ile Leu Val Gly Thr Phe Pro Val Glu
 515 520 525
 Cys Val His Val Lys Ser Ala Val Glu Ile Val Leu Ser Glu Pro Pro
 530 535 540
 His Gln Val Cys Phe Cys Val Phe Phe Ser Phe Glu Met Glu Ser Cys
 545 550 555 560
 Ser Val Pro Gln Leu Glu Leu Gln Lys Ser Pro Val Phe Cys Val Asp
 565 570 575
 His Val Gly Ser Ser Arg Ser Glu Leu Phe Leu Phe Gly His Leu Ser
 580 585 590
 Phe Leu Ser Phe Leu Ser
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<210> 49
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 <212> DNA
 <213> Homo sapiens

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 <223> MOOSE03453

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 Arg Ala Leu Leu Val Gln His Glu Ser Ser Asn Gln Met Phe Ala Met
 20 25 30
 aaa gaa ata agg ctt ccc aag tct ttc tct aat aca cag aat tct agg 144
 Lys Glu Ile Arg Leu Pro Lys Ser Phe Ser Asn Thr Gln Asn Ser Arg
 35 40 45
 aag gag gct gtt ctt tta gcc aaa atg aaa cac cct aat att gtt gcc 192
 Lys Glu Ala Val Leu Leu Ala Lys Met Lys His Pro Asn Ile Val Ala
 50 55 60

87/155

ttc	aaa	gaa	tca	ttt	gaa	gct	gaa	gga	cac	ttg	tat	att	gtg	atg	gaa	240
Phe	Lys	Glu	Ser	Phe	Glu	Ala	Glu	Gly	His	Leu	Tyr	Ile	Val	Met	Glu	
65					70					75					80	
tac	tgt	gat	gga	ggg	gat	cta	atg	caa	aag	att	aaa	cag	cag	aaa	gga	288
Tyr	Cys	Asp	Gly	Gly	Asp	Leu	Met	Gln	Lys	Ile	Lys	Gln	Gln	Lys	Gly	
				85					90					95		
aag	tta	ttt	cct	gaa	gac	atg	ata	ctt	aat	tgg	ttt	acc	caa	atg	tgc	336
Lys	Leu	Phe	Pro	Glu	Asp	Met	Ile	Leu	Asn	Trp	Phe	Thr	Gln	Met	Cys	
			100					105					110			
ctt	gga	gta	aat	cac	att	cac	aag	aaa	cgt	gtg	cta	cac	aga	gat	atc	384
Leu	Gly	Val	Asn	His	Ile	His	Lys	Lys	Arg	Val	Leu	His	Arg	Asp	Ile	
		115					120					125				
aag	tcc	aag	aat	atc	ttc	ctc	act	cag	aat	gga	aaa	gtg	aaa	ttg	gga	432
Lys	Ser	Lys	Asn	Ile	Phe	Leu	Thr	Gln	Asn	Gly	Lys	Val	Lys	Leu	Gly	
	130					135					140					
gac	ttt	gga	tct	gcc	cgt	ctt	ctc	tcc	aat	ccg	atg	gca	ttt	gct	tgt	480
Asp	Phe	Gly	Ser	Ala	Arg	Leu	Leu	Ser	Asn	Pro	Met	Ala	Phe	Ala	Cys	
145					150					155					160	
acc	tat	gtg	gga	act	cct	tat	tat	gtg	cct	cca	gaa	att	tgg	gaa	aac	528
Thr	Tyr	Val	Gly	Thr	Pro	Tyr	Tyr	Val	Pro	Pro	Glu	Ile	Trp	Glu	Asn	
				165					170					175		
ctg	cct	tat	aac	aat	aaa	agt	gac	atc	tgg	tcc	ttg	ggc	tgc	atc	ctg	576
Leu	Pro	Tyr	Asn	Asn	Lys	Ser	Asp	Ile	Trp	Ser	Leu	Gly	Cys	Ile	Leu	
			180					185					190			
tat	gaa	ctc	tgt	acc	ctt	aag	cat	cca	ttt	cag	gca	aat	agt	tgg	aaa	624
Tyr	Glu	Leu	Cys	Thr	Leu	Lys	His	Pro	Phe	Gln	Ala	Asn	Ser	Trp	Lys	
		195					200					205				
aat	ctt	atc	ctc	aaa	gta	tgt	caa	ggg	tgc	atc	agt	cca	ctg	ccg	tct	672
Asn	Leu	Ile	Leu	Lys	Val	Cys	Gln	Gly	Cys	Ile	Ser	Pro	Leu	Pro	Ser	
	210					215					220					
cat	tac	tcc	tat	gaa	ctt	cag	ttc	cta	gtc	aag	cag	atg	ttt	aaa	agg	720
His	Tyr	Ser	Tyr	Glu	Leu	Gln	Phe	Leu	Val	Lys	Gln	Met	Phe	Lys	Arg	
225					230					235					240	
aat	ccc	tca	cat	cgc	ccc	tcg	gct	aca	acg	ctt	ctc	tct	cga	ggc	atc	768
Asn	Pro	Ser	His	Arg	Pro	Ser	Ala	Thr	Thr	Leu	Leu	Ser	Arg	Gly	Ile	
				245					250					255		
gta	gct	cgg	ctt	gtc	cag	aag	tgc	tta	ccc	ccc	gag	gca	atc	tgc	ctg	816
Val	Ala	Arg	Leu	Val	Gln	Lys	Cys	Leu	Pro	Pro	Glu	Ala	Ile	Cys	Leu	
			260					265					270			
tct	cgg	ctt	ccc	aaa	gcg	gga	gga	tcg	cct	gag	cct	ggg	aag	ttg	agg	864
Ser	Arg	Leu	Pro	Lys	Ala	Gly	Gly	Ser	Pro	Glu	Pro	Gly	Lys	Leu	Arg	
		275					280					285				
agg	gca	gtg	agc	tat	gat	cgc	acc	tct	gca	ctc	cag	cct	ggg	caa	cac	912
Arg	Ala	Val	Ser	Tyr	Asp	Arg	Thr	Ser	Ala	Leu	Gln	Pro	Gly	Gln	His	
	290					295					300					

88/155

agc aag act ctg tct caa aaa gaa aag aat ttc cat ccc cta aaa tgt	960
Ser Lys Thr Leu Ser Gln Lys Glu Lys Asn Phe His Pro Leu Lys Cys	
305 310 315 320	
ttc ctt caa gag gaa gaa caa gat aga aag ggt agc cat act gat ttg	1008
Phe Leu Gln Glu Glu Glu Gln Asp Arg Lys Gly Ser His Thr Asp Leu	
325 330 335	
gaa agc att aat gaa aat tta gtt gaa agt gca ttg aga aga gta aac	1056
Glu Ser Ile Asn Glu Asn Leu Val Glu Ser Ala Leu Arg Arg Val Asn	
340 345 350	
aga gaa gaa aaa ggt aat cag ggg ctg gaa gtc agg gta gaa atg aca	1104
Arg Glu Glu Lys Gly Asn Gln Gly Leu Glu Val Arg Val Glu Met Thr	
355 360 365	
agt cag caa agc atc aag agt gag gaa gaa aaa ctc cgg cgg cag caa	1152
Ser Gln Gln Ser Ile Lys Ser Glu Glu Glu Lys Leu Arg Arg Gln Gln	
370 375 380	
cag cga cta cga ggg atg gcg gcg gct gca gca gga act gca aca tcc	1200
Gln Arg Leu Arg Gly Met Ala Ala Ala Ala Ala Gly Thr Ala Thr Ser	
385 390 395 400	
cag agg tgc ata ctg ggg aaa agg ctg aaa aaa gtc tgc aag aag aaa	1248
Gln Arg Cys Ile Leu Gly Lys Arg Leu Lys Lys Val Cys Lys Lys Lys	
405 410 415	
aat caa tac ttt tca ttg agt gat tac tgg atg tca cat aca gat cta	1296
Asn Gln Tyr Phe Ser Leu Ser Asp Tyr Trp Met Ser His Thr Asp Leu	
420 425 430	
ggc aag ccc aac acc ctg gat agc tgg gac tac agg cga cca cca cca	1344
Gly Lys Pro Asn Thr Leu Asp Ser Trp Asp Tyr Arg Arg Pro Pro Pro	
435 440 445	
cgc ccg gcc aat ttt ttt gta ttt tta gta gag atg ggg ttt cac cat	1392
Arg Pro Ala Asn Phe Phe Val Phe Leu Val Glu Met Gly Phe His His	
450 455 460	
gtt agc cag gat ggt ctg ggt gat aag gct tat tct caa act tgc tta	1440
Val Ser Gln Asp Gly Leu Gly Asp Lys Ala Tyr Ser Gln Thr Cys Leu	
465 470 475 480	
tcc cag ttt tgg tat gtg aat agt agg cct att cag tca gca aac agg	1488
Ser Gln Phe Trp Tyr Val Asn Ser Arg Pro Ile Gln Ser Ala Asn Arg	
485 490 495	
aca tct gca ctc tta gca aat tct aga aat tca tgt caa gga tac cag	1536
Thr Ser Ala Leu Leu Ala Asn Ser Arg Asn Ser Cys Gln Gly Tyr Gln	
500 505 510	
atg gaa aaa aaa gat cac tac gtt gca ctc cag cct ggg caa cag agt	1584
Met Glu Lys Lys Asp His Tyr Val Ala Leu Gln Pro Gly Gln Gln Ser	
515 520 525	
gag act ctg tct caa aaa aaa aaa aaa gat tat gtg tgg cta gag	1632
Glu Thr Leu Ser Gln Lys Lys Lys Lys Lys Asp Tyr Val Trp Leu Glu	
530 535 540	

89/155

ttg agg
Leu Arg
545

1638

<210> 50
<211> 546
<212> PRT
<213> Homo sapiens

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20 25 30
Lys Glu Ile Arg Leu Pro Lys Ser Phe Ser Asn Thr Gln Asn Ser Arg
35 40 45
Lys Glu Ala Val Leu Leu Ala Lys Met Lys His Pro Asn Ile Val Ala
50 55 60
Phe Lys Glu Ser Phe Glu Ala Glu Gly His Leu Tyr Ile Val Met Glu
65 70 75 80
Tyr Cys Asp Gly Gly Asp Leu Met Gln Lys Ile Lys Gln Gln Lys Gly
85 90 95
Lys Leu Phe Pro Glu Asp Met Ile Leu Asn Trp Phe Thr Gln Met Cys
100 105 110
Leu Gly Val Asn His Ile His Lys Lys Arg Val Leu His Arg Asp Ile
115 120 125
Lys Ser Lys Asn Ile Phe Leu Thr Gln Asn Gly Lys Val Lys Leu Gly
130 135 140
Asp Phe Gly Ser Ala Arg Leu Leu Ser Asn Pro Met Ala Phe Ala Cys
145 150 155 160
Thr Tyr Val Gly Thr Pro Tyr Tyr Val Pro Pro Glu Ile Trp Glu Asn
165 170 175
Leu Pro Tyr Asn Asn Lys Ser Asp Ile Trp Ser Leu Gly Cys Ile Leu
180 185 190
Tyr Glu Leu Cys Thr Leu Lys His Pro Phe Gln Ala Asn Ser Trp Lys
195 200 205
Asn Leu Ile Leu Lys Val Cys Gln Gly Cys Ile Ser Pro Leu Pro Ser
210 215 220
His Tyr Ser Tyr Glu Leu Gln Phe Leu Val Lys Gln Met Phe Lys Arg
225 230 235 240
Asn Pro Ser His Arg Pro Ser Ala Thr Thr Leu Leu Ser Arg Gly Ile
245 250 255
Val Ala Arg Leu Val Gln Lys Cys Leu Pro Pro Glu Ala Ile Cys Leu
260 265 270
Ser Arg Leu Pro Lys Ala Gly Gly Ser Pro Glu Pro Gly Lys Leu Arg
275 280 285
Arg Ala Val Ser Tyr Asp Arg Thr Ser Ala Leu Gln Pro Gly Gln His
290 295 300
Ser Lys Thr Leu Ser Gln Lys Glu Lys Asn Phe His Pro Leu Lys Cys
305 310 315 320
Phe Leu Gln Glu Glu Glu Gln Asp Arg Lys Gly Ser His Thr Asp Leu
325 330 335
Glu Ser Ile Asn Glu Asn Leu Val Glu Ser Ala Leu Arg Arg Val Asn
340 345 350
Arg Glu Glu Lys Gly Asn Gln Gly Leu Glu Val Arg Val Glu Met Thr
355 360 365
Ser Gln Gln Ser Ile Lys Ser Glu Glu Glu Lys Leu Arg Arg Gln Gln
370 375 380
Gln Arg Leu Arg Gly Met Ala Ala Ala Ala Gly Thr Ala Thr Ser
385 390 395 400

90/155

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<210> 51
<211> 1632
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1) ... (1632)  
<223> MOOSE03455
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<400>	51																
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Tyr	Arg	Asn	Val	Ser	Arg	Ala	His	Glu	Arg	Leu	His	Ser	Cys	Leu	Val		
1				5					10					15			
ggc	ctg	gga	gtg	ttt	ctg	cgg	ggg	gtg	gcc	tac	agg	gct	aag	agg	gag		96
Gly	Leu	Gly	Val	Phe	Leu	Arg	Gly	Val	Ala	Tyr	Arg	Ala	Lys	Arg	Glu		
			20					25					30				
aga	gat	ggg	gaa	tgg	cta	ctc	agt	gga	gca	gtc	aaa	aaa	cac	atg	gca		144
Arg	Asp	Gly	Glu	Trp	Leu	Leu	Ser	Gly	Ala	Val	Lys	Lys	His	Met	Ala		
		35					40					45					
ttg	att	aag	aac	atg	gct	gat	aaa	tat	ctg	aaa	tcc	ttc	cag	cac	caa		192
Leu	Ile	Lys	Asn	Met	Ala	Asp	Lys	Tyr	Leu	Lys	Ser	Phe	Gln	His	Gln		
	50					55					60						
atg	att	cct	ttt	ctt	aca	gag	aat	ggc	agg	ctg	ttt	att	gta	atg	gaa		240
Met	Ile	Pro	Phe	Leu	Thr	Glu	Asn	Gly	Arg	Leu	Phe	Ile	Val	Met	Glu		
65					70				75						80		
tat	tgt	gat	gga	ggg	gat	ctc	atg	aaa	agg	atc	aat	aga	caa	cgg	ggg		288
Tyr	Cys	Asp	Gly	Gly	Asp	Leu	Met	Lys	Arg	Ile	Asn	Arg	Gln	Arg	Gly		
				85					90					95			
gtg	tta	ttt	agt	gaa	gat	cag	atc	ctc	ggg	ttg	ttt	gta	cag	att	tct		336
Val	Leu	Phe	Ser	Glu	Asp	Gln	Ile	Leu	Gly	Trp	Phe	Val	Gln	Ile	Ser		
			100					105					110				

91/155

cta gga cta aaa cat att cat gac agg aag ata tta cac agg gac ata	384
Leu Gly Leu Lys His Ile His Asp Arg Lys Ile Leu His Arg Asp Ile	
115 120 125	
aaa gct cag aac att ttt ctt agc aag aac gga atg gtg gca aag ctt	432
Lys Ala Gln Asn Ile Phe Leu Ser Lys Asn Gly Met Val Ala Lys Leu	
130 135 140	
ggg gac ttt ggt ata gca aga gtc ctg aat aat tcc atg gaa ctt gct	480
Gly Asp Phe Gly Ile Ala Arg Val Leu Asn Asn Ser Met Glu Leu Ala	
145 150 155 160	
cga act tgt att gga aca cct tac tac ctg tcc cca gag atc tgt cag	528
Arg Thr Cys Ile Gly Thr Pro Tyr Tyr Leu Ser Pro Glu Ile Cys Gln	
165 170 175	
aat aaa ccc tac aac aat aaa acg gat att tgg tct ctt ggc tgt gtc	576
Asn Lys Pro Tyr Asn Asn Lys Thr Asp Ile Trp Ser Leu Gly Cys Val	
180 185 190	
tta tat gag ctc tgc aca ctt aaa cat cct ttt gag ggt aac aac tta	624
Leu Tyr Glu Leu Cys Thr Leu Lys His Pro Phe Glu Gly Asn Asn Leu	
195 200 205	
cag cag ctg gtt ctg aag att tgt caa gca cat ttt gcc cca ata tct	672
Gln Gln Leu Val Leu Lys Ile Cys Gln Ala His Phe Ala Pro Ile Ser	
210 215 220	
ccg ggg ttt tct cgt gag ctc cat tcc ttg ata tct cag ctc ttt caa	720
Pro Gly Phe Ser Arg Glu Leu His Ser Leu Ile Ser Gln Leu Phe Gln	
225 230 235 240	
gta tct cct cga gac cga cca tcc ata aat tcc att ttg aaa agg ccc	768
Val Ser Pro Arg Asp Arg Pro Ser Ile Asn Ser Ile Leu Lys Arg Pro	
245 250 255	
ttt tta gag aat ctt att ccc aaa tat ttg act cct gag gta agt ttt	816
Phe Leu Glu Asn Leu Ile Pro Lys Tyr Leu Thr Pro Glu Val Ser Phe	
260 265 270	
gag tac ctt cag aga aaa ttt gaa gct caa caa tat aag ttg aaa gtg	864
Glu Tyr Leu Gln Arg Lys Phe Glu Ala Gln Gln Tyr Lys Leu Lys Val	
275 280 285	
gag aag caa ttg gta agt tct aaa ggc tat tta agg caa aat ctg agt	912
Glu Lys Gln Leu Val Ser Ser Lys Gly Tyr Leu Arg Gln Asn Leu Ser	
290 295 300	
gca gtt gaa ctg att ctt aaa aat ctc tta aag gcg cca cat tgg aaa	960
Ala Val Glu Leu Ile Leu Lys Asn Leu Leu Lys Ala Pro His Trp Lys	
305 310 315 320	
ttc atc ctt cca tct ccc aag aag gtc tct aga gtt ggc aca gat cac	1008
Phe Ile Leu Pro Ser Pro Lys Lys Val Ser Arg Val Gly Thr Asp His	
325 330 335	
tgc ttc ttc aga aga gct tca cat gaa ata gcc agc ctg tac gca cag	1056
Cys Phe Phe Arg Arg Ala Ser His Glu Ile Ala Ser Leu Tyr Ala Gln	
340 345 350	

92/155

ttt	cac	atg	gct	ggg	gag	gcc	tca	caa	tca	tgg	cag	aag	gca	aag	gag	1104
Phe	His	Met	Ala	Gly	Glu	Ala	Ser	Gln	Ser	Trp	Gln	Lys	Ala	Lys	Glu	
		355				360						365				
gag	caa	agt	cat	gcc	tta	cat	gaa	ggc	agg	caa	gag	agc	ttg	tgg	gaa	1152
Glu	Gln	Ser	His	Ala	Leu	His	Glu	Gly	Arg	Gln	Glu	Ser	Leu	Trp	Glu	
	370					375					380					
ctc	cta	ttt	aca	aaa	cca	tca	gat	ctt	cta	aag	gct	gca	gtg	agc	cat	1200
Leu	Leu	Phe	Thr	Lys	Pro	Ser	Asp	Leu	Leu	Lys	Ala	Ala	Val	Ser	His	
	385				390					395					400	
gat	tgt	gcc	act	gta	ccc	cag	cct	ggg	ata	cag	agc	aag	act	cgg	tct	1248
Asp	Cys	Ala	Thr	Val	Pro	Gln	Pro	Gly	Ile	Gln	Ser	Lys	Thr	Arg	Ser	
			405						410					415		
caa	aaa	aat	aaa	gcg	ctc	ctc	aca	tcc	cag	acg	ggg	cgg	cgg	ggc	aaa	1296
Gln	Lys	Asn	Lys	Ala	Leu	Leu	Thr	Ser	Gln	Thr	Gly	Arg	Arg	Gly	Lys	
			420					425					430			
ggc	gct	ccc	cac	atc	tca	gac	gat	ggg	cgg	ccg	ggc	aga	gac	gct	cct	1344
Gly	Ala	Pro	His	Ile	Ser	Asp	Asp	Gly	Arg	Pro	Gly	Arg	Asp	Ala	Pro	
		435					440					445				
cac	ttc	cta	gat	ggg	atg	gcg	gcg	ggg	cag	aga	cgc	tcc	tca	ctt	tcc	1392
His	Phe	Leu	Asp	Gly	Met	Ala	Ala	Gly	Gln	Arg	Arg	Ser	Ser	Leu	Ser	
	450					455					460					
aga	ctg	ggc	agc	cag	gca	gag	ggg	ctc	ctc	acg	tcc	cag	acg	atg	ggc	1440
Arg	Leu	Gly	Ser	Gln	Ala	Glu	Gly	Leu	Leu	Thr	Ser	Gln	Thr	Met	Gly	
	465				470					475					480	
ggc	cgg	gca	gag	acg	ctc	ctc	act	tcc	cag	acg	ggg	ctg	agg	cag	gag	1488
Gly	Arg	Ala	Glu	Thr	Leu	Leu	Thr	Ser	Gln	Thr	Gly	Leu	Arg	Gln	Glu	
			485						490					495		
aat	tgc	ttg	aac	ctg	ggc	ggc	gga	ggg	tgc	agt	gag	cca	aga	tcg	agt	1536
Asn	Cys	Leu	Asn	Leu	Gly	Gly	Gly	Gly	Cys	Ser	Glu	Pro	Arg	Ser	Ser	
			500					505					510			
ggg	gag	aga	ggg	cat	ccc	tgt	ctt	gtg	cca	ggt	ttc	aaa	ggg	aat	gct	1584
Gly	Glu	Arg	Gly	His	Pro	Cys	Leu	Val	Pro	Val	Phe	Lys	Gly	Asn	Ala	
		515				520						525				
tcc	agt	ttt	tgc	cca	ttc	aaa	aac	aaa	gat	gag	gta	agg	tgg	gtc	aga	1632
Ser	Ser	Phe	Cys	Pro	Phe	Lys	Asn	Lys	Asp	Glu	Val	Arg	Trp	Val	Arg	
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<210> 52
 <211> 544
 <212> PRT
 <213> Homo sapiens

<400> 52
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 Gly Leu Gly Val Phe Leu Arg Gly Val Ala Tyr Arg Ala Lys Arg Glu
 20 25 30
 Arg Asp Gly Trp Leu Leu Ser Gly Ala Val Lys Lys His Met Ala
 35 40 45

93/155

Leu	Ile	Lys	Asn	Met	Ala	Asp	Lys	Tyr	Leu	Lys	Ser	Phe	Gln	His	Gln
50						55					60				
Met	Ile	Pro	Phe	Leu	Thr	Glu	Asn	Gly	Arg	Leu	Phe	Ile	Val	Met	Glu
65					70					75					80
Tyr	Cys	Asp	Gly	Gly	Asp	Leu	Met	Lys	Arg	Ile	Asn	Arg	Gln	Arg	Gly
			85						90					95	
Val	Leu	Phe	Ser	Glu	Asp	Gln	Ile	Leu	Gly	Trp	Phe	Val	Gln	Ile	Ser
			100					105					110		
Leu	Gly	Leu	Lys	His	Ile	His	Asp	Arg	Lys	Ile	Leu	His	Arg	Asp	Ile
		115					120					125			
Lys	Ala	Gln	Asn	Ile	Phe	Leu	Ser	Lys	Asn	Gly	Met	Val	Ala	Lys	Leu
	130					135					140				
Gly	Asp	Phe	Gly	Ile	Ala	Arg	Val	Leu	Asn	Asn	Ser	Met	Glu	Leu	Ala
145					150					155					160
Arg	Thr	Cys	Ile	Gly	Thr	Pro	Tyr	Tyr	Leu	Ser	Pro	Glu	Ile	Cys	Gln
			165						170					175	
Asn	Lys	Pro	Tyr	Asn	Asn	Lys	Thr	Asp	Ile	Trp	Ser	Leu	Gly	Cys	Val
		180						185					190		
Leu	Tyr	Glu	Leu	Cys	Thr	Leu	Lys	His	Pro	Phe	Glu	Gly	Asn	Asn	Leu
		195					200					205			
Gln	Gln	Leu	Val	Leu	Lys	Ile	Cys	Gln	Ala	His	Phe	Ala	Pro	Ile	Ser
	210					215					220				
Pro	Gly	Phe	Ser	Arg	Glu	Leu	His	Ser	Leu	Ile	Ser	Gln	Leu	Phe	Gln
225					230					235					240
Val	Ser	Pro	Arg	Asp	Arg	Pro	Ser	Ile	Asn	Ser	Ile	Leu	Lys	Arg	Pro
			245						250					255	
Phe	Leu	Glu	Asn	Leu	Ile	Pro	Lys	Tyr	Leu	Thr	Pro	Glu	Val	Ser	Phe
			260					265					270		
Glu	Tyr	Leu	Gln	Arg	Lys	Phe	Glu	Ala	Gln	Gln	Tyr	Lys	Leu	Lys	Val
	275						280					285			
Glu	Lys	Gln	Leu	Val	Ser	Ser	Lys	Gly	Tyr	Leu	Arg	Gln	Asn	Leu	Ser
	290					295					300				
Ala	Val	Glu	Leu	Ile	Leu	Lys	Asn	Leu	Leu	Lys	Ala	Pro	His	Trp	Lys
305					310					315					320
Phe	Ile	Leu	Pro	Ser	Pro	Lys	Lys	Val	Ser	Arg	Val	Gly	Thr	Asp	His
			325						330					335	
Cys	Phe	Phe	Arg	Arg	Ala	Ser	His	Glu	Ile	Ala	Ser	Leu	Tyr	Ala	Gln
		340						345					350		
Phe	His	Met	Ala	Gly	Glu	Ala	Ser	Gln	Ser	Trp	Gln	Lys	Ala	Lys	Glu
		355					360					365			
Glu	Gln	Ser	His	Ala	Leu	His	Glu	Gly	Arg	Gln	Glu	Ser	Leu	Trp	Glu
	370					375					380				
Leu	Leu	Phe	Thr	Lys	Pro	Ser	Asp	Leu	Leu	Lys	Ala	Ala	Val	Ser	His
385					390					395					400
Asp	Cys	Ala	Thr	Val	Pro	Gln	Pro	Gly	Ile	Gln	Ser	Lys	Thr	Arg	Ser
			405						410					415	
Gln	Lys	Asn	Lys	Ala	Leu	Leu	Thr	Ser	Gln	Thr	Gly	Arg	Arg	Gly	Lys
		420						425					430		
Gly	Ala	Pro	His	Ile	Ser	Asp	Asp	Gly	Arg	Pro	Gly	Arg	Asp	Ala	Pro
		435					440					445			
His	Phe	Leu	Asp	Gly	Met	Ala	Ala	Gly	Gln	Arg	Arg	Ser	Ser	Leu	Ser
	450					455					460				
Arg	Leu	Gly	Ser	Gln	Ala	Glu	Gly	Leu	Leu	Thr	Ser	Gln	Thr	Met	Gly
465					470					475					480
Gly	Arg	Ala	Glu	Thr	Leu	Leu	Thr	Ser	Gln	Thr	Gly	Leu	Arg	Gln	Glu
			485						490					495	
Asn	Cys	Leu	Asn	Leu	Gly	Gly	Gly	Gly	Cys	Ser	Glu	Pro	Arg	Ser	Ser
		500						505					510		
Gly	Glu	Arg	Gly	His	Pro	Cys	Leu	Val	Pro	Val	Phe	Lys	Gly	Asn	Ala
		515					520					525			
Ser	Ser	Phe	Cys	Pro	Phe	Lys	Asn	Lys	Asp	Glu	Val	Arg	Trp	Val	Arg
	530					535					540				

94/155

<210> 53
 <211> 2559
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(2559)
 <223> MOOSE03475

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 Ala Lys Met Lys Val Trp Ala Leu Leu Pro Arg Leu Asp Ser Glu Trp
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ggt atg tgt ccg ggg tgg gag tca ggg gaa ggg gga ggc aga tgg aga 96
 Gly Met Cys Pro Gly Trp Glu Ser Gly Glu Gly Gly Gly Arg Trp Arg
 20 25 30

ggg tgg cag cct cca gct gca tta gag cct cgt gga caa cct agg gaa 144
 Gly Trp Gln Pro Pro Ala Ala Leu Glu Pro Arg Gly Gln Pro Arg Glu
 35 40 45

cat ttc tgc atg gtt cta ggc aga ggc aga tca gcc aaa ggg aga gga 192
 His Phe Cys Met Val Leu Gly Arg Gly Arg Ser Ala Lys Gly Arg Gly
 50 55 60

gct gaa ggt gct tgg aag ggc cag gta gga ggg tgc aga gaa tgt gga 240
 Ala Glu Gly Ala Trp Lys Gly Gln Val Gly Gly Cys Arg Glu Cys Gly
 65 70 75 80

gaa ata gta acg gtt tta cac tgt tgg tgg gag tgt aaa ctg gtt caa 288
 Glu Ile Val Thr Val Leu His Cys Trp Trp Glu Cys Lys Leu Val Gln
 85 90 95

cca ttg tgg aag aca gtg tgg cga ttc ctc aag gat cta gaa cta gaa 336
 Pro Leu Trp Lys Thr Val Trp Arg Phe Leu Lys Asp Leu Glu Leu Glu
 100 105 110

ata cca ttt gac cca gca atc cca ttt ctg ggt ata tac cca aag gat 384
 Ile Pro Phe Asp Pro Ala Ile Pro Phe Leu Gly Ile Tyr Pro Lys Asp
 115 120 125

tat aaa tca tgc tac tat aaa gac aaa tgc aca ctt cat gtc ctt tgc 432
 Tyr Lys Ser Cys Tyr Tyr Lys Asp Lys Cys Thr Leu His Val Leu Cys
 130 135 140

agg gac atg gat gaa gat gga tac cat cat tct gag caa act gtc aca 480
 Arg Asp Met Asp Glu Asp Gly Tyr His His Ser Glu Gln Thr Val Thr
 145 150 155 160

agg aca gaa aac caa aca ctg cat att ctc act cat agg tgg gaa ttg 528
 Arg Thr Glu Asn Gln Thr Leu His Ile Leu Thr His Arg Trp Glu Leu
 165 170 175

aac aat gag aac att tgg aca cag ggt ggg gaa cat cac aaa cgg ggg 576
 Asn Asn Glu Asn Ile Trp Thr Gln Gly Gly Glu His His Lys Arg Gly
 180 185 190

95/155

cct	gtc	atg	gga	tgg	ggg	gca	ggg	gga	ggg	ata	gca	tta	gga	gaa	ata	624
Pro	Val	Met	Gly	Trp	Gly	Ala	Gly	Gly	Gly	Ile	Ala	Leu	Gly	Glu	Ile	
		195					200					205				
cct	aat	gta	aat	gac	gag	tta	atg	ggg	gca	gca	aac	caa	cat	ggc	aca	672
Pro	Asn	Val	Asn	Asp	Glu	Leu	Met	Gly	Ala	Ala	Asn	Gln	His	Gly	Thr	
	210					215					220					
tgt	ata	cct	atg	tat	caa	acc	tgc	acc	tta	ata	tgc	aaa	tgt	ctc	act	720
Cys	Ile	Pro	Met	Tyr	Gln	Thr	Cys	Thr	Leu	Ile	Cys	Lys	Cys	Leu	Thr	
225					230					235					240	
ttt	gat	ttt	tct	tta	gtt	ttg	cta	ctt	gag	aag	ata	gaa	cat	gat	gac	768
Phe	Asp	Phe	Ser	Leu	Val	Leu	Leu	Leu	Glu	Lys	Ile	Glu	His	Asp	Asp	
				245					250					255		
atc	tgc	aat	aaa	act	ttg	aag	att	aca	gat	ttt	ggg	ttg	gcg	agg	gaa	816
Ile	Cys	Asn	Lys	Thr	Leu	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Ala	Arg	Glu	
			260					265					270			
tgg	cac	agg	acc	acc	aaa	atg	agc	aca	gca	ggc	acc	tat	gcc	tgg	atg	864
Trp	His	Arg	Thr	Thr	Lys	Met	Ser	Thr	Ala	Gly	Thr	Tyr	Ala	Trp	Met	
		275					280					285				
gcc	ccc	gaa	gtg	atc	aag	tct	tcc	ttg	ttt	tct	aag	gga	agc	gac	atc	912
Ala	Pro	Glu	Val	Ile	Lys	Ser	Ser	Leu	Phe	Ser	Lys	Gly	Ser	Asp	Ile	
	290					295					300					
tgg	agc	tat	gga	gtg	ctg	ctg	tgg	gaa	ctg	ctc	acc	gga	gaa	gtc	ccc	960
Trp	Ser	Tyr	Gly	Val	Leu	Leu	Trp	Glu	Leu	Leu	Thr	Gly	Glu	Val	Pro	
305					310					315					320	
tat	cgg	ggc	att	gat	ggc	ctc	gcc	gtg	gct	tat	ggg	gta	gca	gtc	aat	1008
Tyr	Arg	Gly	Ile	Asp	Gly	Leu	Ala	Val	Ala	Tyr	Gly	Val	Ala	Val	Asn	
				325				330						335		
aaa	ctc	act	ttg	ccc	att	cca	tcc	acc	tgc	cct	gag	ccg	ttt	gcc	aag	1056
Lys	Leu	Thr	Leu	Pro	Ile	Pro	Ser	Thr	Cys	Pro	Glu	Pro	Phe	Ala	Lys	
			340					345					350			
ctc	atg	aaa	gaa	tgc	tgg	caa	caa	gac	cct	cat	att	cgt	cca	tcg	ttt	1104
Leu	Met	Lys	Glu	Cys	Trp	Gln	Gln	Asp	Pro	His	Ile	Arg	Pro	Ser	Phe	
		355					360					365				
gcc	tta	att	ctc	gaa	cag	ttg	act	gct	att	gaa	ggg	gca	gtg	atg	act	1152
Ala	Leu	Ile	Leu	Glu	Gln	Leu	Thr	Ala	Ile	Glu	Gly	Ala	Val	Met	Thr	
	370					375					380					
gag	atg	cct	caa	gaa	tct	ttt	cat	tcc	atg	caa	gat	gac	tgg	aaa	cta	1200
Glu	Met	Pro	Gln	Glu	Ser	Phe	His	Ser	Met	Gln	Asp	Asp	Trp	Lys	Leu	
385					390					395					400	
gaa	att	caa	caa	atg	ttt	gat	gag	ttg	aga	aca	aag	gaa	aag	gag	ctg	1248
Glu	Ile	Gln	Gln	Met	Phe	Asp	Glu	Leu	Arg	Thr	Lys	Glu	Lys	Glu	Leu	
				405					410					415		
cga	tcc	cgg	gaa	gag	gag	ctg	act	cgg	gcg	gct	ctg	cag	cag	aag	tct	1296
Arg	Ser	Arg	Glu	Glu	Glu	Leu	Thr	Arg	Ala	Ala	Leu	Gln	Gln	Lys	Ser	
			420					425					430			

96/155

cag gag gag ctg cta aag cgg cgt gag cag cag ctg gca gag cgc gag Gln Glu Glu Leu Leu Lys Arg Arg Glu Gln Gln Leu Ala Glu Arg Glu 435 440 445	1344
atc gac gtg ctg gag cgg gaa ctt aac att ctg ata ttc cag cta aac Ile Asp Val Leu Glu Arg Glu Leu Asn Ile Leu Ile Phe Gln Leu Asn 450 455 460	1392
cag gag aag ccc aag gta aag aag agg aag ggc aag ttt aag aga agt Gln Glu Lys Pro Lys Val Lys Lys Arg Lys Gly Lys Phe Lys Arg Ser 465 470 475 480	1440
cgt tta aag ctc aaa gat gga cat cga atc agt tta cct tca gat ttc Arg Leu Lys Leu Lys Asp Gly His Arg Ile Ser Leu Pro Ser Asp Phe 485 490 495	1488
cag cac aag ata acc gtg cag gcc tct ccc aac ttg gac aaa cgg cgg Gln His Lys Ile Thr Val Gln Ala Ser Pro Asn Leu Asp Lys Arg Arg 500 505 510	1536
agc ctg aac agc agc agt tcc agt ccc ccg agc agc ccc aca atg atg Ser Leu Asn Ser Ser Ser Ser Pro Pro Ser Ser Pro Thr Met Met 515 520 525	1584
ccc cga ctc cga gcc ata cag ttg act tca gat gaa agc aat aaa act Pro Arg Leu Arg Ala Ile Gln Leu Thr Ser Asp Glu Ser Asn Lys Thr 530 535 540	1632
tgg gga agg aac aca gtc ttt cga caa gaa gaa ttt gag gat gta aaa Trp Gly Arg Asn Thr Val Phe Arg Gln Glu Glu Phe Glu Asp Val Lys 545 550 555 560	1680
agg aat ttt aag aaa aaa ggt tgt acc tgg gga cca aat tcc att caa Arg Asn Phe Lys Lys Lys Gly Cys Thr Trp Gly Pro Asn Ser Ile Gln 565 570 575	1728
atg aaa gat aga aca gat tgc aaa gaa agg tac gcc tac att gat cta Met Lys Asp Arg Thr Asp Cys Lys Glu Arg Tyr Ala Tyr Ile Asp Leu 580 585 590	1776
cct ctt ggg aaa gat gct cag aga gag aat cct gca gaa gct gaa agc Pro Leu Gly Lys Asp Ala Gln Arg Glu Asn Pro Ala Glu Ala Glu Ser 595 600 605	1824
tgg gag gag gca gcc tct gcg aat gct gcc aca gtc tcc att gag atg Trp Glu Glu Ala Ala Ser Ala Asn Ala Ala Thr Val Ser Ile Glu Met 610 615 620	1872
act cct acg aat agt ctg agt aga tcc ccc cag aga aag aaa acg gag Thr Pro Thr Asn Ser Leu Ser Arg Ser Pro Gln Arg Lys Lys Thr Glu 625 630 635 640	1920
tca gct ctg tat ggg tgc acc gtc ctt ctg gca tcg gtg gct ctg gga Ser Ala Leu Tyr Gly Cys Thr Val Leu Leu Ala Ser Val Ala Leu Gly 645 650 655	1968
ctg gac ctc aga gag ctt cat aaa gca cag gct gct gaa gaa ccg ttg Leu Asp Leu Arg Glu Leu His Lys Ala Gln Ala Ala Glu Glu Pro Leu 660 665 670	2016

97/155

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ccc aag gaa gag aag aag aaa cga gag gga atc ttc cag cgg gct tcc 2064
Pro Lys Glu Glu Lys Lys Lys Arg Glu Gly Ile Phe Gln Arg Ala Ser
      675      680      685

aag tcc cgc aga agc gcc agt cct ccc aca agc ctg cca tcc acc tgt 2112
Lys Ser Arg Arg Ser Ala Ser Pro Pro Thr Ser Leu Pro Ser Thr Cys
      690      695      700

ggg gag gcc agc agc cca ccc tcc ctg cca ctg tca agt gcc ctg ggc 2160
Gly Glu Ala Ser Ser Pro Pro Ser Leu Pro Leu Ser Ser Ala Leu Gly
      705      710      715      720

atc ctc tcc aca cct tct ttc tcc aca aag tgc ctg ctg cag atg gac 2208
Ile Leu Ser Thr Pro Ser Phe Ser Thr Lys Cys Leu Leu Gln Met Asp
      725      730      735

agt gaa gat cca ctg gtg gac agt gca cct gtc act tgt gac tct gag 2256
Ser Glu Asp Pro Leu Val Asp Ser Ala Pro Val Thr Cys Asp Ser Glu
      740      745      750

atg ctc act ccg gat ttt tgt ccc act gcc cca gga agt ggt cgt gag 2304
Met Leu Thr Pro Asp Phe Cys Pro Thr Ala Pro Gly Ser Gly Arg Glu
      755      760      765

cca gcc ctc atg cca aga ctt gac act gat tgt agt gta tca aga aac 2352
Pro Ala Leu Met Pro Arg Leu Asp Thr Asp Cys Ser Val Ser Arg Asn
      770      775      780

ttg ccg tct tcc ttc cta cag cag aca tgt ggg aat gta cct tac tgt 2400
Leu Pro Ser Ser Phe Leu Gln Gln Thr Cys Gly Asn Val Pro Tyr Cys
      785      790      795      800

gct tct tca aaa cat aga ccg tca cat cac aga cgg acc atg tct gat 2448
Ala Ser Ser Lys His Arg Pro Ser His His Arg Arg Thr Met Ser Asp
      805      810      815

gga aat ccg acc cca agt gat cag cct gct agg gct gcc ata aca gag 2496
Gly Asn Pro Thr Pro Ser Asp Gln Pro Ala Arg Ala Ala Ile Thr Glu
      820      825      830

tgc cac agc atg gag aga tgt tca gca caa act cat tgt cca gca gtt 2544
Cys His Ser Met Glu Arg Cys Ser Ala Gln Thr His Cys Pro Ala Val
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cca gag gct gga agt 2559
Pro Glu Ala Gly Ser
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 <213> Homo sapiens

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 Ala Lys Met Lys Val Trp Ala Leu Leu Pro Arg Leu Asp Ser Glu Trp
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 Gly Met Cys Pro Gly Trp Glu Ser Gly Glu Gly Gly Arg Trp Arg
 20 25 30
 Gly Trp Gln Pro Pro Ala Ala Leu Glu Pro Arg Gly Gln Pro Arg Glu
 35 40 45

98/155

His	Phe	Cys	Met	Val	Leu	Gly	Arg	Gly	Arg	Ser	Ala	Lys	Gly	Arg	Gly
	50					55					60				
Ala	Glu	Gly	Ala	Trp	Lys	Gly	Gln	Val	Gly	Gly	Cys	Arg	Glu	Cys	Gly
65					70					75					80
Glu	Ile	Val	Thr	Val	Leu	His	Cys	Trp	Trp	Glu	Cys	Lys	Leu	Val	Gln
			85						90					95	
Pro	Leu	Trp	Lys	Thr	Val	Trp	Arg	Phe	Leu	Lys	Asp	Leu	Glu	Leu	Glu
			100					105					110		
Ile	Pro	Phe	Asp	Pro	Ala	Ile	Pro	Phe	Leu	Gly	Ile	Tyr	Pro	Lys	Asp
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Tyr	Lys	Ser	Cys	Tyr	Tyr	Lys	Asp	Lys	Cys	Thr	Leu	His	Val	Leu	Cys
	130					135					140				
Arg	Asp	Met	Asp	Glu	Asp	Gly	Tyr	His	His	Ser	Glu	Gln	Thr	Val	Thr
145					150					155					160
Arg	Thr	Glu	Asn	Gln	Thr	Leu	His	Ile	Leu	Thr	His	Arg	Trp	Glu	Leu
			165						170					175	
Asn	Asn	Glu	Asn	Ile	Trp	Thr	Gln	Gly	Gly	Glu	His	His	Lys	Arg	Gly
			180					185					190		
Pro	Val	Met	Gly	Trp	Gly	Ala	Gly	Gly	Gly	Ile	Ala	Leu	Gly	Glu	Ile
		195					200					205			
Pro	Asn	Val	Asn	Asp	Glu	Leu	Met	Gly	Ala	Ala	Asn	Gln	His	Gly	Thr
	210					215					220				
Cys	Ile	Pro	Met	Tyr	Gln	Thr	Cys	Thr	Leu	Ile	Cys	Lys	Cys	Leu	Thr
225					230					235					240
Phe	Asp	Phe	Ser	Leu	Val	Leu	Leu	Leu	Glu	Lys	Ile	Glu	His	Asp	Asp
			245						250					255	
Ile	Cys	Asn	Lys	Thr	Leu	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Ala	Arg	Glu
			260					265					270		
Trp	His	Arg	Thr	Thr	Lys	Met	Ser	Thr	Ala	Gly	Thr	Tyr	Ala	Trp	Met
		275					280					285			
Ala	Pro	Glu	Val	Ile	Lys	Ser	Ser	Leu	Phe	Ser	Lys	Gly	Ser	Asp	Ile
	290					295					300				
Trp	Ser	Tyr	Gly	Val	Leu	Leu	Trp	Glu	Leu	Leu	Thr	Gly	Glu	Val	Pro
305					310					315					320
Tyr	Arg	Gly	Ile	Asp	Gly	Leu	Ala	Val	Ala	Tyr	Gly	Val	Ala	Val	Asn
			325					330						335	
Lys	Leu	Thr	Leu	Pro	Ile	Pro	Ser	Thr	Cys	Pro	Glu	Pro	Phe	Ala	Lys
			340					345					350		
Leu	Met	Lys	Glu	Cys	Trp	Gln	Gln	Asp	Pro	His	Ile	Arg	Pro	Ser	Phe
		355					360					365			
Ala	Leu	Ile	Leu	Glu	Gln	Leu	Thr	Ala	Ile	Glu	Gly	Ala	Val	Met	Thr
	370					375					380				
Glu	Met	Pro	Gln	Glu	Ser	Phe	His	Ser	Met	Gln	Asp	Asp	Trp	Lys	Leu
385					390					395					400
Glu	Ile	Gln	Gln	Met	Phe	Asp	Glu	Leu	Arg	Thr	Lys	Glu	Lys	Glu	Leu
			405						410					415	
Arg	Ser	Arg	Glu	Glu	Glu	Leu	Thr	Arg	Ala	Ala	Leu	Gln	Gln	Lys	Ser
			420					425					430		
Gln	Glu	Glu	Leu	Leu	Lys	Arg	Arg	Glu	Gln	Gln	Leu	Ala	Glu	Arg	Glu
		435					440					445			
Ile	Asp	Val	Leu	Glu	Arg	Glu	Leu	Asn	Ile	Leu	Ile	Phe	Gln	Leu	Asn
	450					455					460				
Gln	Glu	Lys	Pro	Lys	Val	Lys	Lys	Arg	Lys	Gly	Lys	Phe	Lys	Arg	Ser
465					470					475					480
Arg	Leu	Lys	Leu	Lys	Asp	Gly	His	Arg	Ile	Ser	Leu	Pro	Ser	Asp	Phe
			485						490					495	
Gln	His	Lys	Ile	Thr	Val	Gln	Ala	Ser	Pro	Asn	Leu	Asp	Lys	Arg	Arg
			500					505					510		
Ser	Leu	Asn	Ser	Ser	Ser	Ser	Ser	Pro	Pro	Ser	Ser	Pro	Thr	Met	Met
		515					520					525			
Pro	Arg	Leu	Arg	Ala	Ile	Gln	Leu	Thr	Ser	Asp	Glu	Ser	Asn	Lys	Thr
	530					535					540				

99/155

Trp Gly Arg Asn Thr Val Phe Arg Gln Glu Glu Phe Glu Asp Val Lys
 545 550 555 560
 Arg Asn Phe Lys Lys Lys Gly Cys Thr Trp Gly Pro Asn Ser Ile Gln
 565 570 575
 Met Lys Asp Arg Thr Asp Cys Lys Glu Arg Tyr Ala Tyr Ile Asp Leu
 580 585 590
 Pro Leu Gly Lys Asp Ala Gln Arg Glu Asn Pro Ala Glu Ala Glu Ser
 595 600 605
 Trp Glu Glu Ala Ala Ser Ala Asn Ala Ala Thr Val Ser Ile Glu Met
 610 615 620
 Thr Pro Thr Asn Ser Leu Ser Arg Ser Pro Gln Arg Lys Lys Thr Glu
 625 630 635 640
 Ser Ala Leu Tyr Gly Cys Thr Val Leu Leu Ala Ser Val Ala Leu Gly
 645 650 655
 Leu Asp Leu Arg Glu Leu His Lys Ala Gln Ala Ala Glu Glu Pro Leu
 660 665 670
 Pro Lys Glu Glu Lys Lys Lys Arg Glu Gly Ile Phe Gln Arg Ala Ser
 675 680 685
 Lys Ser Arg Arg Ser Ala Ser Pro Pro Thr Ser Leu Pro Ser Thr Cys
 690 695 700
 Gly Glu Ala Ser Ser Pro Pro Ser Leu Pro Leu Ser Ser Ala Leu Gly
 705 710 715 720
 Ile Leu Ser Thr Pro Ser Phe Ser Thr Lys Cys Leu Leu Gln Met Asp
 725 730 735
 Ser Glu Asp Pro Leu Val Asp Ser Ala Pro Val Thr Cys Asp Ser Glu
 740 745 750
 Met Leu Thr Pro Asp Phe Cys Pro Thr Ala Pro Gly Ser Gly Arg Glu
 755 760 765
 Pro Ala Leu Met Pro Arg Leu Asp Thr Asp Cys Ser Val Ser Arg Asn
 770 775 780
 Leu Pro Ser Ser Phe Leu Gln Gln Thr Cys Gly Asn Val Pro Tyr Cys
 785 790 795 800
 Ala Ser Ser Lys His Arg Pro Ser His His Arg Arg Thr Met Ser Asp
 805 810 815
 Gly Asn Pro Thr Pro Ser Asp Gln Pro Ala Arg Ala Ala Ile Thr Glu
 820 825 830
 Cys His Ser Met Glu Arg Cys Ser Ala Gln Thr His Cys Pro Ala Val
 835 840 845
 Pro Glu Ala Gly Ser
 850

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 1 5 10 15
 tgc aac ctc tgc ctc tct tgc tca ggt gat ctt ccc acc tca gtc gcc 96
 Cys Asn Leu Cys Leu Ser Cys Ser Gly Asp Leu Pro Thr Ser Val Ala
 20 25 30

100/155

caa agg gaa tgc cag gct ggg gaa gtt tta caa tgt tta ata ggt tgg	144
Gln Arg Glu Cys Gln Ala Gly Glu Val Leu Gln Cys Leu Ile Gly Trp	
35 40 45	
gca ggg aag acc tcc ctg aga ggg tgg cct gag gga gag agg aag aaa	192
Ala Gly Lys Thr Ser Leu Arg Gly Trp Pro Glu Gly Glu Arg Lys Lys	
50 55 60	
act gtg cag acg ttt gga aga agt gag ttc cag gaa gaa gaa aca gca	240
Thr Val Gln Thr Phe Gly Arg Ser Glu Phe Gln Glu Glu Glu Thr Ala	
65 70 75 80	
agt tca ttt tcc tgg aga cgg gag cat gcc tca tgt gtt ctt cat gca	288
Ser Ser Phe Ser Trp Arg Arg Glu His Ala Ser Cys Val Leu His Ala	
85 90 95	
tct gct aga att ttt act tgc atg ttt tac tct gga gtg gag tgg cgc	336
Ser Ala Arg Ile Phe Thr Cys Met Phe Tyr Ser Gly Val Glu Trp Arg	
100 105 110	
gat ctc ggt tca ctg caa cct cca cct ccc ggg ttc aag cga ttc tcc	384
Asp Leu Gly Ser Leu Gln Pro Pro Pro Pro Gly Phe Lys Arg Phe Ser	
115 120 125	
tgc ctc agc ctc cca agt agc tgg gac tac agg tcc ctg cca cca tgc	432
Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg Ser Leu Pro Pro Cys	
130 135 140	
ctg gct aat ttt tgt att ttt aga gat aaa acc aaa ggt gca aaa gtg	480
Leu Ala Asn Phe Cys Ile Phe Arg Asp Lys Thr Lys Gly Ala Lys Val	
145 150 155 160	
gtt gaa act cag gga tgg gag gag gaa gca gag gat ttc tat ttc aat	528
Val Glu Thr Gln Gly Trp Glu Glu Glu Ala Glu Asp Phe Tyr Phe Asn	
165 170 175	
tat aag cct tgt agt act tgg cct cca gct gct tct tca ttt tct cca	576
Tyr Lys Pro Cys Ser Thr Trp Pro Pro Ala Ala Ser Ser Phe Ser Pro	
180 185 190	
ggg ctt ccc tgt gac tgt gga tca ggc cat tgc act cca gtc tgc act	624
Gly Leu Pro Cys Asp Cys Gly Ser Gly His Cys Thr Pro Val Cys Thr	
195 200 205	
gca cct ggt ggt ttg ata ttt tta atc ttt act gat ttt ttt gag tta	672
Ala Pro Gly Gly Leu Ile Phe Leu Ile Phe Thr Asp Phe Phe Glu Leu	
210 215 220	
ttt tta gaa tgg gag gca atg cca ctc tgt ggg cag tgt agc cta ggg	720
Phe Leu Glu Trp Glu Ala Met Pro Leu Cys Gly Gln Cys Ser Leu Gly	
225 230 235 240	
cct agg agg tgt cat cat tgt tct cat ttt aca cac ggg gaa act gag	768
Pro Arg Arg Cys His His Cys Ser His Phe Thr His Gly Glu Thr Glu	
245 250 255	
gct cag gga gta aga tca ctt gct tct ggg att aca gat gca tgc cac	816
Ala Gln Gly Val Arg Ser Leu Ala Ser Gly Ile Thr Asp Ala Cys His	
260 265 270	

101/155

cac	gcc	cag	cta	act	ttt	gta	ttt	tta	gta	cag	acg	ggg	ctt	cac	cat	864
His	Ala	Gln	Leu	Thr	Phe	Val	Phe	Leu	Val	Gln	Thr	Gly	Leu	His	His	
		275					280					285				
gtt	ggc	cag	gct	ggg	ctc	aat	ctc	ttg	act	tca	ggg	gat	ctg	ccc	cct	912
Val	Gly	Gln	Ala	Gly	Leu	Asn	Leu	Leu	Thr	Ser	Gly	Asp	Leu	Pro	Pro	
	290					295					300					
cgg	cct	ctc	caa	atc	cgc	agg	gac	cga	gtg	gaa	ccc	cag	agc	gtg	tcc	960
Arg	Pro	Leu	Gln	Ile	Arg	Arg	Asp	Arg	Val	Glu	Pro	Gln	Ser	Val	Ser	
305					310					315					320	
ctg	tcg	tgg	cgg	gag	ccc	atc	cct	gcc	gga	gcc	cct	ggg	gcc	aat	gac	1008
Leu	Ser	Trp	Arg	Glu	Pro	Ile	Pro	Ala	Gly	Ala	Pro	Gly	Ala	Asn	Asp	
				325					330					335		
acg	gag	tac	gag	atc	cga	tac	tac	gag	aag	ggg	cag	agt	gag	cag	act	1056
Thr	Glu	Tyr	Glu	Ile	Arg	Tyr	Tyr	Glu	Lys	Gly	Gln	Ser	Glu	Gln	Thr	
			340					345					350			
tac	tcc	atg	gtg	aag	aca	ggg	gcg	ccc	aca	gtc	acc	gtc	acc	aac	ctg	1104
Tyr	Ser	Met	Val	Lys	Thr	Gly	Ala	Pro	Thr	Val	Thr	Val	Thr	Asn	Leu	
		355					360					365				
aag	ccg	gct	acc	cgc	tac	gtc	ttt	cag	atc	cgg	gcc	gct	tcc	ccg	ggg	1152
Lys	Pro	Ala	Thr	Arg	Tyr	Val	Phe	Gln	Ile	Arg	Ala	Ala	Ser	Pro	Gly	
	370					375					380					
cca	tcc	tgg	gag	gcc	cag	agt	ttt	aac	ccc	agc	att	gaa	gta	cag	acc	1200
Pro	Ser	Trp	Glu	Ala	Gln	Ser	Phe	Asn	Pro	Ser	Ile	Glu	Val	Gln	Thr	
385					390				395						400	
ctg	ggg	gag	ggg	aag	gac	cag	agc	ccc	gcc	att	gtc	gtc	acc	gta	gtg	1248
Leu	Gly	Glu	Gly	Lys	Asp	Gln	Ser	Pro	Ala	Ile	Val	Val	Thr	Val	Val	
				405					410					415		
acc	atc	tcg	gcc	ctc	ctc	gtc	ctg	ggc	tcc	gtg	atg	agt	gct	ctg	aga	1296
Thr	Ile	Ser	Ala	Leu	Leu	Val	Leu	Gly	Ser	Val	Met	Ser	Ala	Leu	Arg	
			420					425					430			
ggc	aga	agg	agg	aaa	ggg	aga	caa	gca	agc	caa	gag	ccc	ctc	ttc	cgg	1344
Gly	Arg	Arg	Arg	Lys	Gly	Arg	Gln	Ala	Ser	Gln	Glu	Pro	Leu	Phe	Arg	
		435					440					445				
gca	gag	gct	ctg	cag	gac	agg	agc	gcc	cca	ggg	aca	gtc	cca	aca	cgt	1392
Ala	Glu	Ala	Leu	Gln	Asp	Arg	Ser	Ala	Pro	Gly	Thr	Val	Pro	Thr	Arg	
	450				455						460					
cgc	aca	ttc	ctg	gac	ccc	cag	agc	tgt	ggg	gac	ctg	ctg	cag	gct	gtg	1440
Arg	Thr	Phe	Leu	Asp	Pro	Gln	Ser	Cys	Gly	Asp	Leu	Leu	Gln	Ala	Val	
465					470				475						480	
cat	ctg	ttc	gcc	aag	gaa	ctg	gat	gcg	aaa	agc	gtc	acg	ctg	gag	agg	1488
His	Leu	Phe	Ala	Lys	Glu	Leu	Asp	Ala	Lys	Ser	Val	Thr	Leu	Glu	Arg	
				485					490					495		
agc	ctt	gga	gga	ggc	aag	ctg	ggc	gcc	cag	gaa	gcc	ttg	tgc	tgt	ttc	1536
Ser	Leu	Gly	Gly	Gly	Lys	Leu	Gly	Ala	Gln	Glu	Ala	Leu	Cys	Cys	Phe	
			500					505					510			

102/155

ccc Pro	aca Thr	ggg Gly 515	cgg Arg	ttt Phe	ggg Gly	gag Glu 520	ctg Leu	tgc Cys	tgt Cys	ggc Gly	tgc Cys	ttg Leu 525	cag Gln	ctc Leu	ccc Pro	1584
ggt Gly	cgc Arg 530	cag Gln	gag Glu	ctg Leu	ctc Leu	gta Val 535	gcc Ala	gtg Val	cat His	atg Met	ctg Leu 540	agg Arg	gac Asp	agc Ser	gcc Ala	1632
tcc Ser 545	gac Asp	tca Ser	cag Gln	agg Arg	ctc Leu 550	ggc Gly	ttc Phe	ctg Leu	gcc Ala	gag Glu 555	gcc Ala	ctc Leu	acg Thr	ctg Leu	ggc Gly 560	1680
cag Gln	ttt Phe	gac Asp	cat His	agc Ser 565	cac His	atc Ile	gtg Val	cgg Arg	ctg Leu 570	gag Glu	ggc Gly	gtt Val	gtt Val	acc Thr 575	cga Arg	1728
ggt Gly	agg Arg	gcc Ala 580	cgc Arg	acc Thr	ttg Leu	atg Met	att Ile	gtc Val 585	acc Thr	gag Glu	tac Tyr	atg Met	agc Ser 590	cat His	ggg Gly	1776
gcc Ala	ctg Leu	gac Asp 595	ggc Gly	ttc Phe	ctc Leu	agg Arg	cgg Arg 600	cac His	gag Glu	ggg Gly	cag Gln	ctg Leu 605	gtg Val	gct Ala	ggg Gly	1824
caa Gln 610	ctg Leu	atg Met	ggg Gly	ttg Leu	ctg Leu	cct Pro 615	ggg Gly	ctg Leu	gca Ala	tca Ser	gcc Ala 620	atg Met	aag Lys	tat Tyr	ctg Leu	1872
tca Ser 625	gag Glu	atg Met	ggc Gly	tac Tyr	gtt Val 630	cac His	cgg Arg	ggc Gly	ctg Leu	gca Ala 635	gct Ala	cgc Arg	cat His	gtg Val	ctg Leu 640	1920
gtc Val	agc Ser	agc Ser	gac Asp	ctt Leu 645	gtc Val	tgc Cys	aag Lys	atc Ile	tct Ser 650	ggc Gly	ttc Phe	ggg Gly	cgg Arg	ggc Gly 655	ccc Pro	1968
cgg Arg	gac Asp	cga Arg 660	tca Ser	gag Glu	gct Ala	gtc Val	tac Tyr	acc Thr 665	act Thr	atg Met	agt Ser	ggc Gly	cgg Arg 670	agc Ser	cca Pro	2016
gcg Ala	cta Leu	tgg Trp 675	gcc Ala	gct Ala	ccc Pro	gag Glu	aca Thr 680	ctt Leu	cag Gln	ttt Phe	ggc Gly 685	cac His	ttc Phe	agc Ser	tct Ser	2064
gcc Ala 690	agt Ser	gac Asp	gtg Val	tgg Trp	agc Ser	ttc Phe 695	ggc Gly	atc Ile	atc Ile	atg Met	tgg Trp 700	gag Glu	gtg Val	atg Met	gcc Ala	2112
ttt Phe 705	ggg Gly	gag Glu	cgg Arg	cct Pro	tac Tyr 710	tgg Trp	gac Asp	atg Met	tct Ser	ggc Gly 715	caa Gln	gac Asp	gtg Val	atc Ile	aag Lys 720	2160
gct Ala	gtg Val	gag Glu	gat Asp	ggc Gly 725	ttc Phe	cgg Arg	ctg Leu	cca Pro	ccc Pro 730	ccc Pro	agg Arg	aac Asn	tgt Cys	cct Pro 735	aac Asn	2208
ctt Leu	ctg Leu	cac His	cga Arg 740	cta Leu	atg Met	ctc Leu	gac Asp	tgc Cys 745	tgg Trp	cag Gln	aag Lys	gac Asp	cca Pro 750	ggt Gly	gag Glu	2256

103/155

cgg ccc agg ttc tcc cag atc cac agc atc ctg agc aag atg gtg cag	2304
Arg Pro Arg Phe Ser Gln Ile His Ser Ile Leu Ser Lys Met Val Gln	
755 760 765	
gac cca gag ccc ccc aag tat ccc agc tgt cgg ttg agc aca gct cct	2352
Asp Pro Glu Pro Pro Lys Tyr Pro Ser Cys Arg Leu Ser Thr Ala Pro	
770 775 780	
ctg acc cgc agg cct ccc acc cca cta gcg gac cgt gcc ttc tcc acc	2400
Leu Thr Arg Arg Pro Pro Thr Pro Leu Ala Asp Arg Ala Phe Ser Thr	
785 790 795 800	
ttc ccc tcc ttt ggc tct gtg ggc gcg tgg ctg gag gcc ctg gac ctg	2448
Phe Pro Ser Phe Gly Ser Val Gly Ala Trp Leu Glu Ala Leu Asp Leu	
805 810 815	
tgc cgc tac aag gac agc ttc gcg gct gct ggc tat ggg agc ctg gag	2496
Cys Arg Tyr Lys Asp Ser Phe Ala Ala Ala Gly Tyr Gly Ser Leu Glu	
820 825 830	
gcc gtg gcc gag atg act gcc cag gac ctg gtg agc cta ggc atc tct	2544
Ala Val Ala Glu Met Thr Ala Gln Asp Leu Val Ser Leu Gly Ile Ser	
835 840 845	
ttg gct gaa cat cga gag gcc ctc ctc agc ggg atc agc gcc ctg cag	2592
Leu Ala Glu His Arg Glu Ala Leu Leu Ser Gly Ile Ser Ala Leu Gln	
850 855 860	
gca cga gtg ctc cag ctg cag ggc cag ggg gtg	2625
Ala Arg Val Leu Gln Leu Gln Gly Gln Gly Val	
865 870 875	

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Val Ser Leu Gln Pro Arg Leu Glu Cys Ser Gly Ala Ile Ser Ala His	
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Gln Arg Glu Cys Gln Ala Gly Glu Val Leu Gln Cys Leu Ile Gly Trp	
35 40 45	
Ala Gly Lys Thr Ser Leu Arg Gly Trp Pro Glu Gly Glu Arg Lys Lys	
50 55 60	
Thr Val Gln Thr Phe Gly Arg Ser Glu Phe Gln Glu Glu Thr Ala	
65 70 75 80	
Ser Ser Phe Ser Trp Arg Arg Glu His Ala Ser Cys Val Leu His Ala	
85 90 95	
Ser Ala Arg Ile Phe Thr Cys Met Phe Tyr Ser Gly Val Glu Trp Arg	
100 105 110	
Asp Leu Gly Ser Leu Gln Pro Pro Pro Gly Phe Lys Arg Phe Ser	
115 120 125	
Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Arg Ser Leu Pro Pro Cys	
130 135 140	
Leu Ala Asn Phe Cys Ile Phe Arg Asp Lys Thr Lys Gly Ala Lys Val	
145 150 155 160	
Val Glu Thr Gln Gly Trp Glu Glu Glu Ala Glu Asp Phe Tyr Phe Asn	
165 170 175	

104/155

Tyr	Lys	Pro	Cys	Ser	Thr	Trp	Pro	Pro	Ala	Ala	Ser	Ser	Phe	Ser	Pro
			180					185					190		
Gly	Leu	Pro	Cys	Asp	Cys	Gly	Ser	Gly	His	Cys	Thr	Pro	Val	Cys	Thr
		195					200					205			
Ala	Pro	Gly	Gly	Leu	Ile	Phe	Leu	Ile	Phe	Thr	Asp	Phe	Phe	Glu	Leu
	210					215					220				
Phe	Leu	Glu	Trp	Glu	Ala	Met	Pro	Leu	Cys	Gly	Gln	Cys	Ser	Leu	Gly
225					230					235					240
Pro	Arg	Arg	Cys	His	His	Cys	Ser	His	Phe	Thr	His	Gly	Glu	Thr	Glu
				245					250					255	
Ala	Gln	Gly	Val	Arg	Ser	Leu	Ala	Ser	Gly	Ile	Thr	Asp	Ala	Cys	His
			260					265					270		
His	Ala	Gln	Leu	Thr	Phe	Val	Phe	Leu	Val	Gln	Thr	Gly	Leu	His	His
		275					280					285			
Val	Gly	Gln	Ala	Gly	Leu	Asn	Leu	Leu	Thr	Ser	Gly	Asp	Leu	Pro	Pro
	290					295					300				
Arg	Pro	Leu	Gln	Ile	Arg	Arg	Asp	Arg	Val	Glu	Pro	Gln	Ser	Val	Ser
305					310					315					320
Leu	Ser	Trp	Arg	Glu	Pro	Ile	Pro	Ala	Gly	Ala	Pro	Gly	Ala	Asn	Asp
				325					330					335	
Thr	Glu	Tyr	Glu	Ile	Arg	Tyr	Tyr	Glu	Lys	Gly	Gln	Ser	Glu	Gln	Thr
			340					345					350		
Tyr	Ser	Met	Val	Lys	Thr	Gly	Ala	Pro	Thr	Val	Thr	Val	Thr	Asn	Leu
		355					360					365			
Lys	Pro	Ala	Thr	Arg	Tyr	Val	Phe	Gln	Ile	Arg	Ala	Ala	Ser	Pro	Gly
	370					375					380				
Pro	Ser	Trp	Glu	Ala	Gln	Ser	Phe	Asn	Pro	Ser	Ile	Glu	Val	Gln	Thr
385					390					395					400
Leu	Gly	Glu	Gly	Lys	Asp	Gln	Ser	Pro	Ala	Ile	Val	Val	Thr	Val	Val
				405					410					415	
Thr	Ile	Ser	Ala	Leu	Leu	Val	Leu	Gly	Ser	Val	Met	Ser	Ala	Leu	Arg
			420					425					430		
Gly	Arg	Arg	Arg	Lys	Gly	Arg	Gln	Ala	Ser	Gln	Glu	Pro	Leu	Phe	Arg
			435				440					445			
Ala	Glu	Ala	Leu	Gln	Asp	Arg	Ser	Ala	Pro	Gly	Thr	Val	Pro	Thr	Arg
	450					455					460				
Arg	Thr	Phe	Leu	Asp	Pro	Gln	Ser	Cys	Gly	Asp	Leu	Leu	Gln	Ala	Val
465					470					475					480
His	Leu	Phe	Ala	Lys	Glu	Leu	Asp	Ala	Lys	Ser	Val	Thr	Leu	Glu	Arg
				485					490					495	
Ser	Leu	Gly	Gly	Gly	Lys	Leu	Gly	Ala	Gln	Glu	Ala	Leu	Cys	Cys	Phe
			500					505					510		
Pro	Thr	Gly	Arg	Phe	Gly	Glu	Leu	Cys	Cys	Gly	Cys	Leu	Gln	Leu	Pro
		515					520					525			
Gly	Arg	Gln	Glu	Leu	Leu	Val	Ala	Val	His	Met	Leu	Arg	Asp	Ser	Ala
						535					540				
Ser	Asp	Ser	Gln	Arg	Leu	Gly	Phe	Leu	Ala	Glu	Ala	Leu	Thr	Leu	Gly
545					550					555					560
Gln	Phe	Asp	His	Ser	His	Ile	Val	Arg	Leu	Glu	Gly	Val	Val	Thr	Arg
				565					570					575	
Gly	Arg	Ala	Arg	Thr	Leu	Met	Ile	Val	Thr	Glu	Tyr	Met	Ser	His	Gly
			580					585					590		
Ala	Leu	Asp	Gly	Phe	Leu	Arg	Arg	His	Glu	Gly	Gln	Leu	Val	Ala	Gly
		595					600					605			
Gln	Leu	Met	Gly	Leu	Leu	Pro	Gly	Leu	Ala	Ser	Ala	Met	Lys	Tyr	Leu
		610				615					620				
Ser	Glu	Met	Gly	Tyr	Val	His	Arg	Gly	Leu	Ala	Ala	Arg	His	Val	Leu
625					630					635					640
Val	Ser	Ser	Asp	Leu	Val	Cys	Lys	Ile	Ser	Gly	Phe	Gly	Arg	Gly	Pro
				645					650					655	
Arg	Asp	Arg	Ser	Glu	Ala	Val	Tyr	Thr	Thr	Met	Ser	Gly	Arg	Ser	Pro
			660					665					670		

105/155

Ala Leu Trp Ala Ala Pro Glu Thr Leu Gln Phe Gly His Phe Ser Ser
675 680 685
Ala Ser Asp Val Trp Ser Phe Gly Ile Ile Met Trp Glu Val Met Ala
690 695 700
Phe Gly Glu Arg Pro Tyr Trp Asp Met Ser Gly Gln Asp Val Ile Lys
705 710 715 720
Ala Val Glu Asp Gly Phe Arg Leu Pro Pro Arg Asn Cys Pro Asn
725 730 735
Leu Leu His Arg Leu Met Leu Asp Cys Trp Gln Lys Asp Pro Gly Glu
740 745 750
Arg Pro Arg Phe Ser Gln Ile His Ser Ile Leu Ser Lys Met Val Gln
755 760 765
Asp Pro Glu Pro Pro Lys Tyr Pro Ser Cys Arg Leu Ser Thr Ala Pro
770 775 780
Leu Thr Arg Arg Pro Pro Thr Pro Leu Ala Asp Arg Ala Phe Ser Thr
785 790 795 800
Phe Pro Ser Phe Gly Ser Val Gly Ala Trp Leu Glu Ala Leu Asp Leu
805 810 815
Cys Arg Tyr Lys Asp Ser Phe Ala Ala Gly Tyr Gly Ser Leu Glu
820 825 830
Ala Val Ala Glu Met Thr Ala Gln Asp Leu Val Ser Leu Gly Ile Ser
835 840 845
Leu Ala Glu His Arg Glu Ala Leu Leu Ser Gly Ile Ser Ala Leu Gln
850 855 860
Ala Arg Val Leu Gln Leu Gln Gly Gln Gly Val
865 870 875

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<213> Homo sapiens

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<223> MOOSE03608

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tgt ttg ttt gtt tgt ttt gtt ttg ttt tgt ctt ctt aga cat agt ctt 96
Cys Leu Phe Val Cys Phe Val Leu Phe Cys Leu Leu Arg His Ser Leu
20 25 30
gct ctg tcg ccc agg ctg gcg tgc aat gaa acg cta atg gac tcc act 144
Ala Leu Ser Pro Arg Leu Ala Cys Asn Glu Thr Leu Met Asp Ser Thr
35 40 45
aca gcg act gct gag ctg ggc tgg atg gtg cat cct cca tca ggg tgg 192
Thr Ala Thr Ala Glu Leu Gly Trp Met Val His Pro Pro Ser Gly Trp
50 55 60
gaa gag gtg agt ggc tac gat gag aac atg aac acg atc cgc acg tac 240
Glu Glu Val Ser Gly Tyr Asp Glu Asn Met Asn Thr Ile Arg Thr Tyr
65 70 75 80
cag gtg tgc aac gtg ttt gag tca agc cag aac aac tgg cta cgg acc 288
Gln Val Cys Asn Val Phe Glu Ser Ser Gln Asn Asn Trp Leu Arg Thr
85 90 95

106/155

aag ttt atc cgg cgc cgt ggc gcc cac cgc atc cac gtg gag atg aag	336
Lys Phe Ile Arg Arg Arg Gly Ala His Arg Ile His Val Glu Met Lys	
100 105 110	
ttt tcg gtg cgt gac tgc agc agc atc ccc agc gtg cct ggc tcc tgc	384
Phe Ser Val Arg Asp Cys Ser Ser Ile Pro Ser Val Pro Gly Ser Cys	
115 120 125	
aag gag acc ttc aac ctc tat tac tat gag gct gac ttt gac tcg gcc	432
Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu Ala Asp Phe Asp Ser Ala	
130 135 140	
acc aag acc ttc ccc aac tgg atg gag aat cca tgg gtg aag gtg gat	480
Thr Lys Thr Phe Pro Asn Trp Met Glu Asn Pro Trp Val Lys Val Asp	
145 150 155 160	
acc att gca gcc gac gag agc ttc tcc cag gtg gac ctg ggt ggc cgc	528
Thr Ile Ala Ala Asp Glu Ser Phe Ser Gln Val Asp Leu Gly Gly Arg	
165 170 175	
gtc atg aaa atc aac acc gag gtg cgg agc ttc gga cct gtg tcc cgc	576
Val Met Lys Ile Asn Thr Glu Val Arg Ser Phe Gly Pro Val Ser Arg	
180 185 190	
agc ggc ttc tac ctg gcc ttc cag gac tat ggc ggc tgc atg tcc ctc	624
Ser Gly Phe Tyr Leu Ala Phe Gln Asp Tyr Gly Gly Cys Met Ser Leu	
195 200 205	
atc gcc gtg cgt gtc ttc tac cgc aag tgc ccc cgc atc atc cag aat	672
Ile Ala Val Arg Val Phe Tyr Arg Lys Cys Pro Arg Ile Ile Gln Asn	
210 215 220	
ggc gcc atc ttc cag gaa acc ctg tcg ggg gct gag agc aca tcg cta	720
Gly Ala Ile Phe Gln Glu Thr Leu Ser Gly Ala Glu Ser Thr Ser Leu	
225 230 235 240	
gtg gct gcc cgg ggc agc tgc atc gcc aat gcg gaa gag gtg gat gta	768
Val Ala Ala Arg Gly Ser Cys Ile Ala Asn Ala Glu Glu Val Asp Val	
245 250 255	
ccc atc aag ctc tac tgt aac ggg gac ggc gag tgg ctg gtg ccc atc	816
Pro Ile Lys Leu Tyr Cys Asn Gly Asp Gly Glu Trp Leu Val Pro Ile	
260 265 270	
ggg cgc tgc atg tgc aaa gca ggc ttc gag gcc gtt gag aat ggc acc	864
Gly Arg Cys Met Cys Lys Ala Gly Phe Glu Ala Val Glu Asn Gly Thr	
275 280 285	
gtc tgc cga gag gta cac cct ggt gct aag aag gct gtg aag gtt gaa	912
Val Cys Arg Glu Val His Pro Gly Ala Lys Lys Ala Val Lys Val Glu	
290 295 300	
gga cct ggg tta aat cac ccc ttc cac tca cta gcg aca gcc tgg agt	960
Gly Pro Gly Leu Asn His Pro Phe His Ser Leu Ala Thr Ala Trp Ser	
305 310 315 320	
ggg gca tcc acc tgt gct ggg gaa gag gag agg cga gat caa agg atc	1008
Gly Ala Ser Thr Cys Ala Gly Glu Glu Arg Arg Arg Asp Gln Arg Ile	
325 330 335	

107/155

cca gcc ccc cca tcc act gag tgt gag cgt gca cca tca tgc cca gct	1056
Pro Ala Pro Pro Ser Thr Glu Cys Glu Arg Ala Pro Ser Cys Pro Ala	
340 345 350	
aat ttt ttg act gct ccc tct tct ggg acc tca ctg gct ccc agg gtc	1104
Asn Phe Leu Thr Ala Pro Ser Ser Gly Thr Ser Leu Ala Pro Arg Val	
355 360 365	
cca ccc ccc tcc acc tct cgc tct gag ccc ttt gtg gct agt tcc tgt	1152
Pro Pro Pro Ser Thr Ser Arg Ser Glu Pro Phe Val Ala Ser Ser Cys	
370 375 380	
tca tct ccc gac ctc tcc acc ttg gag ggc ccc agt gct gtg tcc ttg	1200
Ser Ser Pro Asp Leu Ser Thr Leu Glu Gly Pro Ser Ala Val Ser Leu	
385 390 395 400	
gcc tcc tct tct ctc tcc ctg atg act cca ccc agc ccc aca gct tca	1248
Ala Ser Ser Ser Leu Ser Leu Met Thr Pro Pro Ser Pro Thr Ala Ser	
405 410 415	
aat gcc ttc tct ggg ctg atc tct agc cca gac ctc tat tct gaa gtg	1296
Asn Ala Phe Ser Gly Leu Ile Ser Ser Pro Asp Leu Tyr Ser Glu Val	
420 425 430	
tgt gtt tgc atg ggt gcc cac cca ctc aca ggg aaa tca gcc aga gta	1344
Cys Val Cys Met Gly Ala His Pro Leu Thr Gly Lys Ser Ala Arg Val	
435 440 445	
ttc aga ttc atg tgt aca tct gta tat ttt atc aag cca gat gta cgt	1392
Phe Arg Phe Met Cys Thr Ser Val Tyr Phe Ile Lys Pro Asp Val Arg	
450 455 460	
gaa aat ggg tac ttg tta gca tat gag gtg gat ttc agg ccc tca ggg	1440
Glu Asn Gly Tyr Leu Leu Ala Tyr Glu Val Asp Phe Arg Pro Ser Gly	
465 470 475 480	
gaa gca aga tct gga att tct gtg gtg gtg cta ggc aca ttc cat aca	1488
Glu Ala Arg Ser Gly Ile Ser Val Val Val Leu Gly Thr Phe His Thr	
485 490 495	
cat ctt cac caa tcc ctg gga gca gga gtt gcc cac ccc gtc tta caa	1536
His Leu His Gln Ser Leu Gly Ala Gly Val Ala His Pro Val Leu Gln	
500 505 510	
gtg aga aaa cag ggc ttg tgc ggt ctc aca gag cac att aat gga act	1584
Val Arg Lys Gln Gly Leu Cys Gly Leu Thr Glu His Ile Asn Gly Thr	
515 520 525	
gcc ttt tac act cag gac cgc att aga cct ttc cca cca tcc cag gct	1632
Ala Phe Tyr Thr Gln Asp Arg Ile Arg Pro Phe Pro Pro Ser Gln Ala	
530 535 540	
gcc gcg gcc agt gta gga atg agc tta ttg ggt tgg ctg gtt tgc cga	1680
Ala Ala Ala Ser Val Gly Met Ser Leu Leu Gly Trp Leu Val Cys Arg	
545 550 555 560	
gat ggt gcc act gca ctc cag cct ggc cgg cag agc aag act gtc aca	1728
Asp Gly Ala Thr Ala Leu Gln Pro Gly Arg Gln Ser Lys Thr Val Thr	
565 570 575	

108/155

aaa	aaa	aaa	gaa	aaa	gaa	aaa	gaa	aag	aaa	agc	aaa	ttc	cag	gaa	agg	1776
Lys	Lys	Lys	Glu	Lys	Glu	Lys	Glu	Lys	Lys	Ser	Lys	Phe	Gln	Glu	Arg	
			580					585					590			
gag	ctg	gtg	gat	tgc	ttg	gcc	att	gag	cct	ccc	ctt	cgt	gct	gcc	ctc	1824
Glu	Leu	Val	Asp	Cys	Leu	Ala	Ile	Glu	Pro	Pro	Leu	Arg	Ala	Ala	Leu	
		595					600					605				
cag	gag	ctt	cac	atc	cac	cta	atg	aag	gaa	att	ggg	ggc	ggg	gcc	tgt	1872
Gln	Glu	Leu	His	Ile	His	Leu	Met	Lys	Glu	Ile	Gly	Gly	Gly	Ala	Cys	
	610					615					620					
gga	gag	cga	gac	gtt	gcc	tgt	gaa	ggc	agg	agg	gag	ggg	act	tca	ggg	1920
Gly	Glu	Arg	Asp	Val	Ala	Cys	Glu	Gly	Arg	Arg	Glu	Gly	Thr	Ser	Gly	
					630				635						640	
cag	cca	gag	gga	gag	gga	cgt	ggc	ccc	aca	gcc	aga	agg	gcc	att	cat	1968
Gln	Pro	Glu	Gly	Glu	Gly	Arg	Gly	Pro	Thr	Ala	Arg	Arg	Ala	Ile	His	
				645					650					655		
gtt	gag	ctg	ggt	cct	ggc	ctc	agg	ctc	tct	gag	cct	cag	caa	ttc	aca	2016
Val	Glu	Leu	Gly	Pro	Gly	Leu	Arg	Leu	Ser	Glu	Pro	Gln	Gln	Phe	Thr	
			660					665					670			
ctc	tgg	gta	ttt	tgt	ctt	cct	ggg	gca	ctg	ccg	gca	ggg	cta	gga	tat	2064
Leu	Trp	Val	Phe	Cys	Leu	Pro	Gly	Ala	Leu	Pro	Ala	Gly	Leu	Gly	Tyr	
		675					680					685				
ttc	tgc	aca	aag	ggc	ctg	tgc	cac	agg	agg	ttg	acc	tcg	aga	tgg	gca	2112
Phe	Cys	Thr	Lys	Gly	Leu	Cys	His	Arg	Arg	Leu	Thr	Ser	Arg	Trp	Ala	
	690					695					700					
gct	gag	gtg	ggt	gct	ggc	aga	ggc	tgt	gga	ggg	gcc	atc	tgg	gag	gta	2160
Ala	Glu	Val	Gly	Ala	Gly	Arg	Gly	Cys	Gly	Gly	Ala	Ile	Trp	Glu	Val	
	705				710				715						720	
ggg	tca	gca	gta	ggc	acc	acg	agg	cat	tgg	gag	atg	ggt	ggg	cat	gcc	2208
Gly	Ser	Ala	Val	Gly	Thr	Thr	Arg	His	Trp	Glu	Met	Gly	Gly	His	Ala	
				725					730					735		
cgg	att	ttc	ctg	aat	gaa	gtt	ggt	ctc	cct	gcg	ccc	cct	gcc	tgc	cct	2256
Arg	Ile	Phe	Leu	Asn	Glu	Val	Gly	Leu	Pro	Ala	Pro	Pro	Ala	Cys	Pro	
			740					745					750			
ctt	ccc	cat	cca	gcc	att	ccc	ctc	tgg	cag	ctc	cag	aac	cat	ctt	tct	2304
Leu	Pro	His	Pro	Ala	Ile	Pro	Leu	Trp	Gln	Leu	Gln	Asn	His	Leu	Ser	
		755					760					765				
aaa	atg	gaa	atc	tgc	atg	ccc	tca	agc	ctt	gat	cat	cac	tgc	gac	aac	2352
Lys	Met	Glu	Ile	Cys	Met	Pro	Ser	Ser	Leu	Asp	His	His	Cys	Asp	Asn	
	770					775					780					
cac	agc	tgc	att	tct	gag	tgc	cat	ctg	ggg	gac	acc	atg	cca	ggc	aag	2400
His	Ser	Cys	Ile	Ser	Glu	Cys	His	Leu	Gly	Asp	Thr	Met	Pro	Gly	Lys	
	785				790					795					800	
acc	cac	tgt	ttc	tca	cgt	tgg	ctc	tgg	ctc	agt	gca	ata	acg	aaa	aca	2448
Thr	His	Cys	Phe	Ser	Arg	Trp	Leu	Trp	Leu	Ser	Ala	Ile	Thr	Lys	Thr	
				805					810					815		

109/155

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agg gca ata ata atg ggg ttt cac cac gtt ggc cag gct ggt ctc aaa 2496
Arg Ala Ile Ile Met Gly Phe His His Val Gly Gln Ala Gly Leu Lys
      820      825      830

ctc ctg gcc tca agt gat ctc ctc acc ttg gcc tcc cta agt gct ggg 2544
Leu Leu Ala Ser Ser Asp Leu Leu Thr Leu Ala Ser Leu Ser Ala Gly
      835      840      845

att ata ggt gtg agc cac cga aga gaa agc ata ttc act att cat tca 2592
Ile Ile Gly Val Ser His Arg Arg Glu Ser Ile Phe Thr Ile His Ser
      850      855      860

gtg gaa gta gat tgt cat aaa ggt cat cct cct cgt ctt 2631
Val Glu Val Asp Cys His Lys Gly His Pro Pro Arg Leu
865      870      875

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 <212> PRT
 <213> Homo sapiens

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Cys Leu Phe Val Cys Phe Val Leu Phe Cys Leu Leu Arg His Ser Leu
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Ala Leu Ser Pro Arg Leu Ala Cys Asn Glu Thr Leu Met Asp Ser Thr
      35      40      45
Thr Ala Thr Ala Glu Leu Gly Trp Met Val His Pro Pro Ser Gly Trp
      50      55      60
Glu Glu Val Ser Gly Tyr Asp Glu Asn Met Asn Thr Ile Arg Thr Tyr
      65      70      75      80
Gln Val Cys Asn Val Phe Glu Ser Ser Gln Asn Asn Trp Leu Arg Thr
      85      90      95
Lys Phe Ile Arg Arg Gly Ala His Arg Ile His Val Glu Met Lys
      100      105      110
Phe Ser Val Arg Asp Cys Ser Ser Ile Pro Ser Val Pro Gly Ser Cys
      115      120      125
Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu Ala Asp Phe Asp Ser Ala
      130      135      140
Thr Lys Thr Phe Pro Asn Trp Met Glu Asn Pro Trp Val Lys Val Asp
      145      150      155      160
Thr Ile Ala Ala Asp Glu Ser Phe Ser Gln Val Asp Leu Gly Gly Arg
      165      170      175
Val Met Lys Ile Asn Thr Glu Val Arg Ser Phe Gly Pro Val Ser Arg
      180      185      190
Ser Gly Phe Tyr Leu Ala Phe Gln Asp Tyr Gly Gly Cys Met Ser Leu
      195      200      205
Ile Ala Val Arg Val Phe Tyr Arg Lys Cys Pro Arg Ile Ile Gln Asn
      210      215      220
Gly Ala Ile Phe Gln Glu Thr Leu Ser Gly Ala Glu Ser Thr Ser Leu
      225      230      235      240
Val Ala Ala Arg Gly Ser Cys Ile Ala Asn Ala Glu Glu Val Asp Val
      245      250      255
Pro Ile Lys Leu Tyr Cys Asn Gly Asp Gly Glu Trp Leu Val Pro Ile
      260      265      270
Gly Arg Cys Met Cys Lys Ala Gly Phe Glu Ala Val Glu Asn Gly Thr
      275      280      285
Val Cys Arg Glu Val His Pro Gly Ala Lys Lys Ala Val Lys Val Glu
      290      295      300

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110/155

Gly	Pro	Gly	Leu	Asn	His	Pro	Phe	His	Ser	Leu	Ala	Thr	Ala	Trp	Ser	305	310	315	320
Gly	Ala	Ser	Thr	Cys	Ala	Gly	Glu	Glu	Glu	Arg	Arg	Asp	Gln	Arg	Ile	325	330	335	
Pro	Ala	Pro	Pro	Ser	Thr	Glu	Cys	Glu	Arg	Ala	Pro	Ser	Cys	Pro	Ala	340	345	350	
Asn	Phe	Leu	Thr	Ala	Pro	Ser	Ser	Gly	Thr	Ser	Leu	Ala	Pro	Arg	Val	355	360	365	
Pro	Pro	Pro	Ser	Thr	Ser	Arg	Ser	Glu	Pro	Phe	Val	Ala	Ser	Ser	Cys	370	375	380	
Ser	Ser	Pro	Asp	Leu	Ser	Thr	Leu	Glu	Gly	Pro	Ser	Ala	Val	Ser	Leu	385	390	395	400
Ala	Ser	Ser	Ser	Leu	Ser	Leu	Met	Thr	Pro	Pro	Ser	Pro	Thr	Ala	Ser	405	410	415	
Asn	Ala	Phe	Ser	Gly	Leu	Ile	Ser	Ser	Pro	Asp	Leu	Tyr	Ser	Glu	Val	420	425	430	
Cys	Val	Cys	Met	Gly	Ala	His	Pro	Leu	Thr	Gly	Lys	Ser	Ala	Arg	Val	435	440	445	
Phe	Arg	Phe	Met	Cys	Thr	Ser	Val	Tyr	Phe	Ile	Lys	Pro	Asp	Val	Arg	450	455	460	
Glu	Asn	Gly	Tyr	Leu	Leu	Ala	Tyr	Glu	Val	Asp	Phe	Arg	Pro	Ser	Gly	465	470	475	480
Glu	Ala	Arg	Ser	Gly	Ile	Ser	Val	Val	Val	Leu	Gly	Thr	Phe	His	Thr	485	490	495	
His	Leu	His	Gln	Ser	Leu	Gly	Ala	Gly	Val	Ala	His	Pro	Val	Leu	Gln	500	505	510	
Val	Arg	Lys	Gln	Gly	Leu	Cys	Gly	Leu	Thr	Glu	His	Ile	Asn	Gly	Thr	515	520	525	
Ala	Phe	Tyr	Thr	Gln	Asp	Arg	Ile	Arg	Pro	Phe	Pro	Pro	Ser	Gln	Ala	530	535	540	
Ala	Ala	Ala	Ser	Val	Gly	Met	Ser	Leu	Leu	Gly	Trp	Leu	Val	Cys	Arg	545	550	555	560
Asp	Gly	Ala	Thr	Ala	Leu	Gln	Pro	Gly	Arg	Gln	Ser	Lys	Thr	Val	Thr	565	570	575	
Lys	Lys	Lys	Glu	Lys	Glu	Lys	Glu	Lys	Lys	Ser	Lys	Phe	Gln	Glu	Arg	580	585	590	
Glu	Leu	Val	Asp	Cys	Leu	Ala	Ile	Glu	Pro	Pro	Leu	Arg	Ala	Ala	Leu	595	600	605	
Gln	Glu	Leu	His	Ile	His	Leu	Met	Lys	Glu	Ile	Gly	Gly	Gly	Ala	Cys	610	615	620	
Gly	Glu	Arg	Asp	Val	Ala	Cys	Glu	Gly	Arg	Arg	Glu	Gly	Thr	Ser	Gly	625	630	635	640
Gln	Pro	Glu	Gly	Glu	Gly	Arg	Gly	Pro	Thr	Ala	Arg	Arg	Ala	Ile	His	645	650	655	
Val	Glu	Leu	Gly	Pro	Gly	Leu	Arg	Leu	Ser	Glu	Pro	Gln	Gln	Phe	Thr	660	665	670	
Leu	Trp	Val	Phe	Cys	Leu	Pro	Gly	Ala	Leu	Pro	Ala	Gly	Leu	Gly	Tyr	675	680	685	
Phe	Cys	Thr	Lys	Gly	Leu	Cys	His	Arg	Arg	Leu	Thr	Ser	Arg	Trp	Ala	690	695	700	
Ala	Glu	Val	Gly	Ala	Gly	Arg	Gly	Cys	Gly	Gly	Ala	Ile	Trp	Glu	Val	705	710	715	720
Gly	Ser	Ala	Val	Gly	Thr	Thr	Arg	His	Trp	Glu	Met	Gly	Gly	His	Ala	725	730	735	
Arg	Ile	Phe	Leu	Asn	Glu	Val	Gly	Leu	Pro	Ala	Pro	Pro	Ala	Cys	Pro	740	745	750	
Leu	Pro	His	Pro	Ala	Ile	Pro	Leu	Trp	Gln	Leu	Gln	Asn	His	Leu	Ser	755	760	765	
Lys	Met	Glu	Ile	Cys	Met	Pro	Ser	Ser	Leu	Asp	His	His	Cys	Asp	Asn	770	775	780	
His	Ser	Cys	Ile	Ser	Glu	Cys	His	Leu	Gly	Asp	Thr	Met	Pro	Gly	Lys	785	790	795	800

Thr	His	Cys	Phe	Ser	Arg	Trp	Leu	Trp	Leu	Ser	Ala	Ile	Thr	Lys	Thr
				805					810					815	
Arg	Ala	Ile	Ile	Met	Gly	Phe	His	His	Val	Gly	Gln	Ala	Gly	Leu	Lys
			820					825					830		
Leu	Leu	Ala	Ser	Ser	Asp	Leu	Leu	Thr	Leu	Ala	Ser	Leu	Ser	Ala	Gly
		835					840					845			
Ile	Ile	Gly	Val	Ser	His	Arg	Arg	Glu	Ser	Ile	Phe	Thr	Ile	His	Ser
	850					855					860				
Val	Glu	Val	Asp	Cys	His	Lys	Gly	His	Pro	Pro	Arg	Leu			
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<222> (1) ... (3930)
<223> MOOSE03639
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				5					10				15				
ttc	ctc	tcc	ttg	gga	ttt	ggc	ctg	gat	aca	gta	gag	gtg	tgc	ccc	agc	96	
Phe	Leu	Ser	Leu	Gly	Phe	Gly	Leu	Asp	Thr	Val	Glu	Val	Cys	Pro	Ser		
				20					25				30				
ctg	gat	att	cgc	tca	gag	gtg	gca	gag	ctt	cgt	cag	ctg	gag	aac	tgc	144	
Leu	Asp	Ile	Arg	Ser	Glu	Val	Ala	Glu	Leu	Arg	Gln	Leu	Glu	Asn	Cys		
				35					40				45				
agc	gtg	gtg	gag	ggc	cac	ctg	cag	atc	ctg	ctc	atg	ttc	aca	gcc	acc	192	
Ser	Val	Val	Glu	Gly	His	Leu	Gln	Ile	Leu	Leu	Met	Phe	Thr	Ala	Thr		
				50					55				60				
ggg	gag	gac	ttc	cgc	ggc	ctc	agc	ttc	cct	cgc	ctc	acc	cag	gtc	acc	240	
Gly	Glu	Asp	Phe	Arg	Gly	Leu	Ser	Phe	Pro	Arg	Leu	Thr	Gln	Val	Thr	80	
				65					70				75				
gac	tac	ctg	ctg	ctc	ttc	cgt	gtc	tac	gga	ctg	gag	agc	ctg	cgc	gac	288	
Asp	Tyr	Leu	Leu	Leu	Phe	Arg	Val	Tyr	Gly	Leu	Glu	Ser	Leu	Arg	Asp		
				85					90				95				
ctc	ttc	ccc	aac	cta	gca	gtc	atc	cgc	ggg	acg	cgc	ctc	ttc	ctg	ggc	336	
Leu	Phe	Pro	Asn	Leu	Ala	Val	Ile	Arg	Gly	Thr	Arg	Leu	Phe	Leu	Gly		
				100					105				110				
tat	gca	ctg	gtc	atc	ttt	gag	atg	cca	cat	ctg	cgt	gac	gtg	gca	ctg	384	
Tyr	Ala	Leu	Val	Ile	Phe	Glu	Met	Pro	His	Leu	Arg	Asp	Val	Ala	Leu		
				115					120				125				
cct	gca	ctt	ggg	gcc	gtg	ctg	cgt	ggg	gct	gtg	cgt	gtg	gag	aag	aac	432	
Pro	Ala	Leu	Gly	Ala	Val	Leu	Arg	Gly	Ala	Val	Arg	Val	Glu	Lys	Asn		
				130					135				140				
cag	gag	ctc	tgc	cac	ctc	tcc	acc	att	gac	tgg	gga	ctg	ctg	cag	cca	480	
Gln	Glu	Leu	Cys	His	Leu	Ser	Thr	Ile	Asp	Trp	Gly	Leu	Leu	Gln	Pro	160	
				145	150				155				160				

112/155

gca	cct	ggc	gcc	aac	cac	atc	gtg	ggc	aac	aag	ctg	ggc	gag	gag	tgt	528
Ala	Pro	Gly	Ala	Asn	His	Ile	Val	Gly	Asn	Lys	Leu	Gly	Glu	Glu	Cys	
				165					170					175		
gct	gac	gtg	tgc	cct	ggg	gtg	ctg	ggg	gct	gct	ggg	gag	ccc	tgt	gcc	576
Ala	Asp	Val	Cys	Pro	Gly	Val	Leu	Gly	Ala	Ala	Gly	Glu	Pro	Cys	Ala	
			180					185					190			
aag	acc	acc	ttc	agc	ggg	cac	act	gac	tac	aga	tgc	tgg	acc	tcc	agc	624
Lys	Thr	Thr	Phe	Ser	Gly	His	Thr	Asp	Tyr	Arg	Cys	Trp	Thr	Ser	Ser	
		195					200					205				
cac	tgc	cag	aga	gtg	tgc	ccc	tgc	ccc	cat	ggg	atg	gct	tgc	aca	gcg	672
His	Cys	Gln	Arg	Val	Cys	Pro	Cys	Pro	His	Gly	Met	Ala	Cys	Thr	Ala	
	210					215					220					
agg	ggc	gag	tgc	tgc	cac	acc	gaa	tgc	ctg	ggg	ggc	tgc	agc	cag	cca	720
Arg	Gly	Glu	Cys	Cys	His	Thr	Glu	Cys	Leu	Gly	Gly	Cys	Ser	Gln	Pro	
225					230					235					240	
gaa	gac	cct	cgt	gcc	tgt	gta	gct	tgc	cgc	cac	ctc	tac	ttc	cag	ggg	768
Glu	Asp	Pro	Arg	Ala	Cys	Val	Ala	Cys	Arg	His	Leu	Tyr	Phe	Gln	Gly	
				245					250					255		
gcc	tgc	ctg	tgg	gcc	tgc	ccg	cca	ggc	acc	tac	cag	tat	gag	tcc	tgg	816
Ala	Cys	Leu	Trp	Ala	Cys	Pro	Pro	Gly	Thr	Tyr	Gln	Tyr	Glu	Ser	Trp	
			260					265					270			
cgc	tgt	gtc	aca	gct	gag	cgc	tgt	gcc	agc	ctg	cac	tct	gtg	ccc	ggc	864
Arg	Cys	Val	Thr	Ala	Glu	Arg	Cys	Ala	Ser	Leu	His	Ser	Val	Pro	Gly	
		275					280					285				
cgt	gcc	tcc	acc	ttc	ggc	ata	cac	cag	ggc	agt	tgc	ctg	gcc	cag	tgc	912
Arg	Ala	Ser	Thr	Phe	Gly	Ile	His	Gln	Gly	Ser	Cys	Leu	Ala	Gln	Cys	
	290					295					300					
cct	tct	ggc	ttc	acc	cgt	aat	agc	agc	agc	ata	ttc	tgc	cac	aag	tgc	960
Pro	Ser	Gly	Phe	Thr	Arg	Asn	Ser	Ser	Ser	Ile	Phe	Cys	His	Lys	Cys	
305					310					315					320	
gag	ggg	ctg	tgc	cct	aaa	gag	tgc	aag	gta	ggc	acc	aag	acc	atc	gac	1008
Glu	Gly	Leu	Cys	Pro	Lys	Glu	Cys	Lys	Val	Gly	Thr	Lys	Thr	Ile	Asp	
				325					330					335		
tcc	atc	cag	gcg	gca	cag	gat	ctt	gtg	ggc	tgc	acg	cat	gtg	gag	gga	1056
Ser	Ile	Gln	Ala	Ala	Gln	Asp	Leu	Val	Gly	Cys	Thr	His	Val	Glu	Gly	
			340					345					350			
agc	ctc	atc	ctc	aac	ctt	cgc	cag	ggc	tac	aac	ctg	gag	cca	cag	ctg	1104
Ser	Leu	Ile	Leu	Asn	Leu	Arg	Gln	Gly	Tyr	Asn	Leu	Glu	Pro	Gln	Leu	
		355					360					365				
cag	cac	agc	ctg	ggg	ctg	gta	gaa	acc	att	act	ggc	ttc	ctc	aaa	atc	1152
Gln	His	Ser	Leu	Gly	Leu	Val	Glu	Thr	Ile	Thr	Gly	Phe	Leu	Lys	Ile	
		370				375					380					
aag	cac	tcc	ttt	gcc	ctc	gtg	tcc	ctg	ggc	ttt	ttc	aag	aac	ctc	aaa	1200
Lys	His	Ser	Phe	Ala	Leu	Val	Ser	Leu	Gly	Phe	Phe	Lys	Asn	Leu	Lys	
385					390					395					400	

113/155

cta atc cgg gga gac gcc atg gtg gat ggg aac tac act ctc tac gtg	1248
Leu Ile Arg Gly Asp Ala Met Val Asp Gly Asn Tyr Thr Leu Tyr Val	
405 410 415	
ctg gac aac cag aac cta caa cag cta ggg tcc tgg gtg gcc gcg ggg	1296
Leu Asp Asn Gln Asn Leu Gln Gln Leu Gly Ser Trp Val Ala Ala Gly	
420 425 430	
ctc acc att ccc gtg ggc aag atc tac ttc gcc ttc aac ccg cgc ctc	1344
Leu Thr Ile Pro Val Gly Lys Ile Tyr Phe Ala Phe Asn Pro Arg Leu	
435 440 445	
tgc ttg gaa cac atc tac cga ctg gag gag gtg aca ggc acg cga ggt	1392
Cys Leu Glu His Ile Tyr Arg Leu Glu Glu Val Thr Gly Thr Arg Gly	
450 455 460	
cgg cag aac aag gct gag atc aac ccc cgc acc aac gga gac cgc gcc	1440
Arg Gln Asn Lys Ala Glu Ile Asn Pro Arg Thr Asn Gly Asp Arg Ala	
465 470 475 480	
gcc tgc cag act cgc acc ctg cgc ttc gtg tcc aac gtg acg gag gca	1488
Ala Cys Gln Thr Arg Thr Leu Arg Phe Val Ser Asn Val Thr Glu Ala	
485 490 495	
gac cgc atc ctg cta cgc tgg gag cgc tat gag cca ctg gag gcc cgc	1536
Asp Arg Ile Leu Leu Arg Trp Glu Arg Tyr Glu Pro Leu Glu Ala Arg	
500 505 510	
gac ctg ctc agc ttc atc gtg tac tac aag gag tcc cca ttc cag aac	1584
Asp Leu Leu Ser Phe Ile Val Tyr Tyr Lys Glu Ser Pro Phe Gln Asn	
515 520 525	
gcc aca gag cac gtg ggt cca gat gct tgt gga acc cag agc tgg aac	1632
Ala Thr Glu His Val Gly Pro Asp Ala Cys Gly Thr Gln Ser Trp Asn	
530 535 540	
ctg ctg gat gtg gag ctg ccc cta agc cgc acc cag gag cca ggg gtg	1680
Leu Leu Asp Val Glu Leu Pro Leu Ser Arg Thr Gln Glu Pro Gly Val	
545 550 555 560	
acc cta gcc tcc ctc aag cct tgg aca cag tac gca gtg ttt gtg cgg	1728
Thr Leu Ala Ser Leu Lys Pro Trp Thr Gln Tyr Ala Val Phe Val Arg	
565 570 575	
gcc atc acg cta acc act gag gag gac agc cct cat caa gga gcc cag	1776
Ala Ile Thr Leu Thr Thr Glu Glu Asp Ser Pro His Gln Gly Ala Gln	
580 585 590	
agt ccc atc gtc tac ctc cga acg ctg cct gca gct ccc acg gtg ccc	1824
Ser Pro Ile Val Tyr Leu Arg Thr Leu Pro Ala Ala Pro Thr Val Pro	
595 600 605	
caa gac gtc atc tcc acg tcc aac tcc tcc tcc cac ctc ctg gtg cgc	1872
Gln Asp Val Ile Ser Thr Ser Asn Ser Ser Ser His Leu Leu Val Arg	
610 615 620	
tgg aag cca ccg acc cag cgc aat ggg aac ctc acc tac tac ctg gtg	1920
Trp Lys Pro Pro Thr Gln Arg Asn Gly Asn Leu Thr Tyr Tyr Leu Val	
625 630 635 640	

114/155

ctg	tgg	cag	cgg	ctg	gca	gag	gac	ggc	gac	ctc	tac	ctc	aat	gac	tac	1968
Leu	Trp	Gln	Arg	Leu	Ala	Glu	Asp	Gly	Asp	Leu	Tyr	Leu	Asn	Asp	Tyr	
				645					650					655		
tgc	cac	cgc	ggc	ttg	cgg	ctg	ccc	acc	agc	aac	aac	gat	ccg	cgc	ttc	2016
Cys	His	Arg	Gly	Leu	Arg	Leu	Pro	Thr	Ser	Asn	Asn	Asp	Pro	Arg	Phe	
			660					665					670			
gac	ggc	gaa	gac	ggg	gat	cct	gag	gcc	gag	atg	gag	tcc	gac	tgc	tgc	2064
Asp	Gly	Glu	Asp	Gly	Asp	Pro	Glu	Ala	Glu	Met	Glu	Ser	Asp	Cys	Cys	
		675					680					685				
cct	tgc	cag	cac	cca	cct	cct	ggt	cag	gtt	ctg	ccc	ccg	ctg	gag	gcg	2112
Pro	Cys	Gln	His	Pro	Pro	Pro	Gly	Gln	Val	Leu	Pro	Pro	Leu	Glu	Ala	
	690					695					700					
caa	gag	gcc	tcg	ttc	cag	aag	aag	ttt	gaa	aac	ttt	cta	cac	aac	gcg	2160
Gln	Glu	Ala	Ser	Phe	Gln	Lys	Lys	Phe	Glu	Asn	Phe	Leu	His	Asn	Ala	
705				710				715							720	
atc	acc	atc	ccc	ata	tcc	cct	tgg	aag	gtg	acg	tcc	atc	aac	aag	agc	2208
Ile	Thr	Ile	Pro	Ile	Ser	Pro	Trp	Lys	Val	Thr	Ser	Ile	Asn	Lys	Ser	
				725				730						735		
ccc	caa	agg	gac	tca	ggg	cgg	cac	cgc	cgg	gca	gct	ggg	ccc	ctc	cgg	2256
Pro	Gln	Arg	Asp	Ser	Gly	Arg	His	Arg	Arg	Ala	Ala	Gly	Pro	Leu	Arg	
			740					745					750			
ctg	ggg	ggc	aac	agc	tcg	gat	ttc	gag	atc	cag	gag	gac	aag	gtg	ccc	2304
Leu	Gly	Gly	Asn	Ser	Ser	Asp	Phe	Glu	Ile	Gln	Glu	Asp	Lys	Val	Pro	
		755					760					765				
cgt	gag	cga	gcg	gtg	ctg	agc	ggc	ctg	cgc	cac	ttc	acg	gaa	tac	cgg	2352
Arg	Glu	Arg	Ala	Val	Leu	Ser	Gly	Leu	Arg	His	Phe	Thr	Glu	Tyr	Arg	
	770					775					780					
atc	gac	atc	cat	gcc	tgc	aac	cac	gcg	gcg	cac	acc	gtg	ggc	tgc	agc	2400
Ile	Asp	Ile	His	Ala	Cys	Asn	His	Ala	Ala	His	Thr	Val	Gly	Cys	Ser	
785				790				795							800	
gcc	gcc	acc	ttc	gtc	ttt	gcg	cgc	acc	atg	ccc	cac	aga	gag	gct	gat	2448
Ala	Ala	Thr	Phe	Val	Phe	Ala	Arg	Thr	Met	Pro	His	Arg	Glu	Ala	Asp	
				805				810						815		
ggt	att	cca	gga	aag	gtg	gcc	tgg	gag	gcc	tcc	agc	aag	aac	agt	gtc	2496
Gly	Ile	Pro	Gly	Lys	Val	Ala	Trp	Glu	Ala	Ser	Ser	Lys	Asn	Ser	Val	
			820					825					830			
ctt	ctg	cgc	tgg	ctc	gag	cca	cca	gac	ccc	aac	gga	ctc	atc	ctc	aag	2544
Leu	Leu	Arg	Trp	Leu	Glu	Pro	Pro	Asp	Pro	Asn	Gly	Leu	Ile	Leu	Lys	
		835					840					845				
tac	gaa	atc	aag	tac	cgc	cgc	ttg	gga	gag	gag	gcc	aca	gtg	ctg	tgt	2592
Tyr	Glu	Ile	Lys	Tyr	Arg	Arg	Leu	Gly	Glu	Glu	Ala	Thr	Val	Leu	Cys	
	850					855					860					
gtg	tcc	cgt	ctt	cga	tat	gcg	aag	ttt	ggg	gga	gtc	cac	ctg	gcc	ctg	2640
Val	Ser	Arg	Leu	Arg	Tyr	Ala	Lys	Phe	Gly	Gly	Val	His	Leu	Ala	Leu	
865					870					875					880	

115/155

ctg	ccc	cct	gga	aac	tac	tct	gcc	agg	gtt	agg	gca	acc	tca	ctg	gct	2688
Leu	Pro	Pro	Gly	Asn	Tyr	Ser	Ala	Arg	Val	Arg	Ala	Thr	Ser	Leu	Ala	
				885					890					895		
ggc	aat	ggc	tct	tgg	aca	gac	agt	gtt	gcc	ttc	tac	atc	ctt	ggc	cca	2736
Gly	Asn	Gly	Ser	Trp	Thr	Asp	Ser	Val	Ala	Phe	Tyr	Ile	Leu	Gly	Pro	
			900					905					910			
gag	gag	gag	gat	gct	ggg	ggg	ctg	cat	gtc	ctc	ctc	act	gcc	acc	cct	2784
Glu	Glu	Glu	Asp	Ala	Gly	Gly	Leu	His	Val	Leu	Leu	Thr	Ala	Thr	Pro	
			915				920					925				
gtg	ggg	ctc	acg	ctg	ctc	atc	gtt	ctt	gct	gcc	ctt	ggg	ttc	ttc	tac	2832
Val	Gly	Leu	Thr	Leu	Leu	Ile	Val	Leu	Ala	Ala	Leu	Gly	Phe	Phe	Tyr	
	930					935					940					
ggc	aag	aag	aga	aac	aga	acc	ctg	tat	gct	tct	gtg	aat	cca	gag	tac	2880
Gly	Lys	Lys	Arg	Asn	Arg	Thr	Leu	Tyr	Ala	Ser	Val	Asn	Pro	Glu	Tyr	
	945				950					955					960	
ttc	agc	gcc	tct	gat	agt	agg	tct	ggg	atg	tat	gtc	cct	gat	gaa	tgg	2928
Phe	Ser	Ala	Ser	Asp	Ser	Arg	Ser	Gly	Met	Tyr	Val	Pro	Asp	Glu	Trp	
				965					970					975		
gag	gtg	cct	cgg	gag	cag	atc	tcg	ata	atc	cgg	gaa	ctg	ggc	cag	ggc	2976
Glu	Val	Pro	Arg	Glu	Gln	Ile	Ser	Ile	Ile	Arg	Glu	Leu	Gly	Gln	Gly	
			980					985					990			
tct	ttt	ggg	atg	gta	tat	gag	ggg	ctg	gca	cga	gga	ctt	gag	gct	gga	3024
Ser	Phe	Gly	Met	Val	Tyr	Glu	Gly	Leu	Ala	Arg	Gly	Leu	Glu	Ala	Gly	
		995					1000					1005				
gag	gag	tcc	aca	ccc	gtg	gcc	ctg	aag	acg	gtg	aat	gag	ctg	gcc	agc	3072
Glu	Glu	Ser	Thr	Pro	Val	Ala	Leu	Lys	Thr	Val	Asn	Glu	Leu	Ala	Ser	
		1010				1015					1020					
cca	cgg	gaa	tgc	att	gag	ttc	ctc	aag	gaa	gct	tct	gtc	atg	aaa	gcc	3120
Pro	Arg	Glu	Cys	Ile	Glu	Phe	Leu	Lys	Glu	Ala	Ser	Val	Met	Lys	Ala	
		1025				1030				1035					1040	
ttc	aag	tgt	cac	cat	gtg	gtg	cgt	ctc	ctg	ggg	gtg	gta	tct	cag	ggc	3168
Phe	Lys	Cys	His	His	Val	Val	Arg	Leu	Leu	Gly	Val	Val	Ser	Gln	Gly	
				1045					1050					1055		
cag	cca	act	ctg	gtc	atc	atg	gag	tta	atg	acc	cgt	ggg	gac	ctc	aag	3216
Gln	Pro	Thr	Leu	Val	Ile	Met	Glu	Leu	Met	Thr	Arg	Gly	Asp	Leu	Lys	
			1060					1065					1070			
agc	cat	ctt	cga	tct	ttg	cgg	cct	gag	gca	gag	aac	aac	cct	ggg	ctc	3264
Ser	His	Leu	Arg	Ser	Leu	Arg	Pro	Glu	Ala	Glu	Asn	Asn	Pro	Gly	Leu	
			1075				1080					1085				
cca	cag	cca	gca	ttg	ggg	gaa	atg	atc	caa	atg	gct	ggg	gag	att	gca	3312
Pro	Gln	Pro	Ala	Leu	Gly		Met	Ile	Gln	Met	Ala	Gly	Glu	Ile	Ala	
		1090				1095					1100					
gac	ggc	atg	gcc	tac	ctt	gct	gcc	aac	aag	ttt	gtg	cac	cga	gat	cta	3360
Asp	Gly	Met	Ala	Tyr	Leu	Ala	Ala	Asn	Lys	Phe	Val	His	Arg	Asp	Leu	
	1105				1110					1115					1120	

116/155

gca gcc cgc aac tgc atg gtg tcc cag gac ttc acc gtc aag atc ggg	3408
Ala Ala Arg Asn Cys Met Val Ser Gln Asp Phe Thr Val Lys Ile Gly	
1125 1130 1135	
gac ttc ggg atg act cgg gac gtg tat gag aca gac tat tac cgc aag	3456
Asp Phe Gly Met Thr Arg Asp Val Tyr Glu Thr Asp Tyr Tyr Arg Lys	
1140 1145 1150	
ggt ggg aag ggg ctg ctg ccc gtg cgc tgg atg gcc ccc gag tcc ctc	3504
Gly Gly Lys Gly Leu Leu Pro Val Arg Trp Met Ala Pro Glu Ser Leu	
1155 1160 1165	
aaa gat ggg atc ttc acc acc cac tcg gat gtc tgg tcc ttt ggc gtg	3552
Lys Asp Gly Ile Phe Thr Thr His Ser Asp Val Trp Ser Phe Gly Val	
1170 1175 1180	
gta ctc tgg gag att gtg acc ctg gca gaa caa ccc tac cag ggc ctg	3600
Val Leu Trp Glu Ile Val Thr Leu Ala Glu Gln Pro Tyr Gln Gly Leu	
1185 1190 1195 1200	
tcc aat gag cag gtg ctg aag ttc gtc atg gat ggc ggg gtc ctg gag	3648
Ser Asn Glu Gln Val Leu Lys Phe Val Met Asp Gly Gly Val Leu Glu	
1205 1210 1215	
gag ctg gag ggc tgt ccc ctt cag ctg cag gag ctg atg agc cgc tgc	3696
Glu Leu Glu Gly Cys Pro Leu Gln Leu Gln Glu Leu Met Ser Arg Cys	
1220 1225 1230	
tgg cag ccg aac cca cgc ctg cgc cca tct ttc aca cac att ctg gac	3744
Trp Gln Pro Asn Pro Arg Leu Arg Pro Ser Phe Thr His Ile Leu Asp	
1235 1240 1245	
agc ata cag gag gag ctg cgg ccc tcc ttc cgc ctc ctc tcc ttc tac	3792
Ser Ile Gln Glu Glu Leu Arg Pro Ser Phe Arg Leu Leu Ser Phe Tyr	
1250 1255 1260	
tac agc ccg gaa tgc cgg ggg gcc cgg ggc tcc ctg cct acc acc gat	3840
Tyr Ser Pro Glu Cys Arg Gly Ala Arg Gly Ser Leu Pro Thr Thr Asp	
1265 1270 1275 1280	
gca gag cct gac tcc tca ccc act cca aga gac tgc agc cct caa aat	3888
Ala Glu Pro Asp Ser Ser Pro Thr Pro Arg Asp Cys Ser Pro Gln Asn	
1285 1290 1295	
ggg gga ggc aga ggt tgc aga gag ccg aga tcg cac cat tgc	3930
Gly Gly Gly Arg Gly Cys Arg Glu Pro Arg Ser His His Cys	
1300 1305 1310	

<210> 60
 <211> 1310
 <212> PRT
 <213> Homo sapiens

<400> 60
 Met Ala Val Pro Ser Leu Trp Pro Trp Gly Ala Cys Leu Pro Val Ile
 1 5 10 15
 Phe Leu Ser Leu Gly Phe Gly Leu Asp Thr Val Glu Val Cys Pro Ser
 20 25 30
 Leu Asp Ile Arg Ser Glu Val Ala Glu Leu Arg Gln Leu Glu Asn Cys
 35 40 45

117/155

Ser	Val	Val	Glu	Gly	His	Leu	Gln	Ile	Leu	Leu	Met	Phe	Thr	Ala	Thr
	50					55					60				
Gly	Glu	Asp	Phe	Arg	Gly	Leu	Ser	Phe	Pro	Arg	Leu	Thr	Gln	Val	Thr
65					70					75					80
Asp	Tyr	Leu	Leu	Leu	Phe	Arg	Val	Tyr	Gly	Leu	Glu	Ser	Leu	Arg	Asp
				85					90					95	
Leu	Phe	Pro	Asn	Leu	Ala	Val	Ile	Arg	Gly	Thr	Arg	Leu	Phe	Leu	Gly
			100					105					110		
Tyr	Ala	Leu	Val	Ile	Phe	Glu	Met	Pro	His	Leu	Arg	Asp	Val	Ala	Leu
	115						120					125			
Pro	Ala	Leu	Gly	Ala	Val	Leu	Arg	Gly	Ala	Val	Arg	Val	Glu	Lys	Asn
	130					135					140				
Gln	Glu	Leu	Cys	His	Leu	Ser	Thr	Ile	Asp	Trp	Gly	Leu	Leu	Gln	Pro
145					150					155					160
Ala	Pro	Gly	Ala	Asn	His	Ile	Val	Gly	Asn	Lys	Leu	Gly	Glu	Glu	Cys
				165					170					175	
Ala	Asp	Val	Cys	Pro	Gly	Val	Leu	Gly	Ala	Ala	Gly	Glu	Pro	Cys	Ala
			180					185					190		
Lys	Thr	Thr	Phe	Ser	Gly	His	Thr	Asp	Tyr	Arg	Cys	Trp	Thr	Ser	Ser
	195						200					205			
His	Cys	Gln	Arg	Val	Cys	Pro	Cys	Pro	His	Gly	Met	Ala	Cys	Thr	Ala
	210					215					220				
Arg	Gly	Glu	Cys	Cys	His	Thr	Glu	Cys	Leu	Gly	Gly	Cys	Ser	Gln	Pro
225					230					235					240
Glu	Asp	Pro	Arg	Ala	Cys	Val	Ala	Cys	Arg	His	Leu	Tyr	Phe	Gln	Gly
				245					250					255	
Ala	Cys	Leu	Trp	Ala	Cys	Pro	Pro	Gly	Thr	Tyr	Gln	Tyr	Glu	Ser	Trp
			260					265					270		
Arg	Cys	Val	Thr	Ala	Glu	Arg	Cys	Ala	Ser	Leu	His	Ser	Val	Pro	Gly
	275						280						285		
Arg	Ala	Ser	Thr	Phe	Gly	Ile	His	Gln	Gly	Ser	Cys	Leu	Ala	Gln	Cys
	290					295					300				
Pro	Ser	Gly	Phe	Thr	Arg	Asn	Ser	Ser	Ser	Ile	Phe	Cys	His	Lys	Cys
305					310					315					320
Glu	Gly	Leu	Cys	Pro	Lys	Glu	Cys	Lys	Val	Gly	Thr	Lys	Thr	Ile	Asp
				325					330					335	
Ser	Ile	Gln	Ala	Gln	Asp	Leu	Val	Gly	Cys	Thr	His	Val	Glu	Gly	
			340					345					350		
Ser	Leu	Ile	Leu	Asn	Leu	Arg	Gln	Gly	Tyr	Asn	Leu	Glu	Pro	Gln	Leu
	355						360						365		
Gln	His	Ser	Leu	Gly	Leu	Val	Glu	Thr	Ile	Thr	Gly	Phe	Leu	Lys	Ile
	370					375					380				
Lys	His	Ser	Phe	Ala	Leu	Val	Ser	Leu	Gly	Phe	Phe	Lys	Asn	Leu	Lys
385					390					395					400
Leu	Ile	Arg	Gly	Asp	Ala	Met	Val	Asp	Gly	Asn	Tyr	Thr	Leu	Tyr	Val
				405					410					415	
Leu	Asp	Asn	Gln	Asn	Leu	Gln	Gln	Leu	Gly	Ser	Trp	Val	Ala	Ala	Gly
			420					425					430		
Leu	Thr	Ile	Pro	Val	Gly	Lys	Ile	Tyr	Phe	Ala	Phe	Asn	Pro	Arg	Leu
	435						440					445			
Cys	Leu	Glu	His	Ile	Tyr	Arg	Leu	Glu	Glu	Val	Thr	Gly	Thr	Arg	Gly
	450					455					460				
Arg	Gln	Asn	Lys	Ala	Glu	Ile	Asn	Pro	Arg	Thr	Asn	Gly	Asp	Arg	Ala
465					470					475					480
Ala	Cys	Gln	Thr	Arg	Thr	Leu	Arg	Phe	Val	Ser	Asn	Val	Thr	Glu	Ala
				485					490					495	
Asp	Arg	Ile	Leu	Leu	Arg	Trp	Glu	Arg	Tyr	Glu	Pro	Leu	Glu	Ala	Arg
			500					505					510		
Asp	Leu	Leu	Ser	Phe	Ile	Val	Tyr	Tyr	Lys	Glu	Ser	Pro	Phe	Gln	Asn
	515						520					525			
Ala	Thr	Glu	His	Val	Gly	Pro	Asp	Ala	Cys	Gly	Thr	Gln	Ser	Trp	Asn
	530					535					540				

118/155

Leu	Leu	Asp	Val	Glu	Leu	Pro	Leu	Ser	Arg	Thr	Gln	Glu	Pro	Gly	Val
545					550					555					560
Thr	Leu	Ala	Ser	Leu	Lys	Pro	Trp	Thr	Gln	Tyr	Ala	Val	Phe	Val	Arg
				565					570					575	
Ala	Ile	Thr	Leu	Thr	Thr	Glu	Glu	Asp	Ser	Pro	His	Gln	Gly	Ala	Gln
			580					585					590		
Ser	Pro	Ile	Val	Tyr	Leu	Arg	Thr	Leu	Pro	Ala	Ala	Pro	Thr	Val	Pro
		595					600					605			
Gln	Asp	Val	Ile	Ser	Thr	Ser	Asn	Ser	Ser	Ser	His	Leu	Leu	Val	Arg
	610					615					620				
Trp	Lys	Pro	Pro	Thr	Gln	Arg	Asn	Gly	Asn	Leu	Thr	Tyr	Tyr	Leu	Val
625					630					635					640
Leu	Trp	Gln	Arg	Leu	Ala	Glu	Asp	Gly	Asp	Leu	Tyr	Leu	Asn	Asp	Tyr
				645					650					655	
Cys	His	Arg	Gly	Leu	Arg	Leu	Pro	Thr	Ser	Asn	Asn	Asp	Pro	Arg	Phe
			660					665					670		
Asp	Gly	Glu	Asp	Gly	Asp	Pro	Glu	Ala	Glu	Met	Glu	Ser	Asp	Cys	Cys
		675					680					685			
Pro	Cys	Gln	His	Pro	Pro	Pro	Gly	Gln	Val	Leu	Pro	Pro	Leu	Glu	Ala
	690					695					700				
Gln	Glu	Ala	Ser	Phe	Gln	Lys	Lys	Phe	Glu	Asn	Phe	Leu	His	Asn	Ala
705					710					715					720
Ile	Thr	Ile	Pro	Ile	Ser	Pro	Trp	Lys	Val	Thr	Ser	Ile	Asn	Lys	Ser
				725					730					735	
Pro	Gln	Arg	Asp	Ser	Gly	Arg	His	Arg	Arg	Ala	Ala	Gly	Pro	Leu	Arg
			740					745					750		
Leu	Gly	Gly	Asn	Ser	Ser	Asp	Phe	Glu	Ile	Gln	Glu	Asp	Lys	Val	Pro
		755					760					765			
Arg	Glu	Arg	Ala	Val	Leu	Ser	Gly	Leu	Arg	His	Phe	Thr	Glu	Tyr	Arg
	770					775					780				
Ile	Asp	Ile	His	Ala	Cys	Asn	His	Ala	Ala	His	Thr	Val	Gly	Cys	Ser
785					790					795					800
Ala	Ala	Thr	Phe	Val	Phe	Ala	Arg	Thr	Met	Pro	His	Arg	Glu	Ala	Asp
			805						810					815	
Gly	Ile	Pro	Gly	Lys	Val	Ala	Trp	Glu	Ala	Ser	Ser	Lys	Asn	Ser	Val
			820					825					830		
Leu	Leu	Arg	Trp	Leu	Glu	Pro	Pro	Asp	Pro	Asn	Gly	Leu	Ile	Leu	Lys
		835					840					845			
Tyr	Glu	Ile	Lys	Tyr	Arg	Arg	Leu	Gly	Glu	Glu	Ala	Thr	Val	Leu	Cys
	850					855					860				
Val	Ser	Arg	Leu	Arg	Tyr	Ala	Lys	Phe	Gly	Gly	Val	His	Leu	Ala	Leu
865					870					875					880
Leu	Pro	Pro	Gly	Asn	Tyr	Ser	Ala	Arg	Val	Arg	Ala	Thr	Ser	Leu	Ala
				885					890					895	
Gly	Asn	Gly	Ser	Trp	Thr	Asp	Ser	Val	Ala	Phe	Tyr	Ile	Leu	Gly	Pro
			900					905					910		
Glu	Glu	Glu	Asp	Ala	Gly	Gly	Leu	His	Val	Leu	Leu	Thr	Ala	Thr	Pro
		915					920					925			
Val	Gly	Leu	Thr	Leu	Leu	Ile	Val	Leu	Ala	Ala	Leu	Gly	Phe	Phe	Tyr
	930					935					940				
Gly	Lys	Lys	Arg	Asn	Arg	Thr	Leu	Tyr	Ala	Ser	Val	Asn	Pro	Glu	Tyr
945					950					955					960
Phe	Ser	Ala	Ser	Asp	Ser	Arg	Ser	Gly	Met	Tyr	Val	Pro	Asp	Glu	Trp
				965					970					975	
Glu	Val	Pro	Arg	Glu	Gln	Ile	Ser	Ile	Ile	Arg	Glu	Leu	Gly	Gln	Gly
			980					985					990		
Ser	Phe	Gly	Met	Val	Tyr	Glu	Gly	Leu	Ala	Arg	Gly	Leu	Glu	Ala	Gly
		995					1000					1005			
Glu	Glu	Ser	Thr	Pro	Val	Ala	Leu	Lys	Thr	Val	Asn	Glu	Leu	Ala	Ser
	1010					1015					1020				
Pro	Arg	Glu	Cys	Ile	Glu	Phe	Leu	Lys	Glu	Ala	Ser	Val	Met	Lys	Ala
1025					1030					1035					1040

Phe	Lys	Cys	His	His	Val	Val	Arg	Leu	Leu	Gly	Val	Val	Ser	Gln	Gly
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Gln	Pro	Thr	Leu	Val	Ile	Met	Glu	Leu	Met	Thr	Arg	Gly	Asp	Leu	Lys
				1060					1065					1070	
Ser	His	Leu	Arg	Ser	Leu	Arg	Pro	Glu	Ala	Glu	Asn	Asn	Pro	Gly	Leu
				1075					1080					1085	
Pro	Gln	Pro	Ala	Leu	Gly	Glu	Met	Ile	Gln	Met	Ala	Gly	Glu	Ile	Ala
				1090					1095					1100	
Asp	Gly	Met	Ala	Tyr	Leu	Ala	Ala	Asn	Lys	Phe	Val	His	Arg	Asp	Leu
1105					1110					1115					1120
Ala	Ala	Arg	Asn	Cys	Met	Val	Ser	Gln	Asp	Phe	Thr	Val	Lys	Ile	Gly
				1125					1130					1135	
Asp	Phe	Gly	Met	Thr	Arg	Asp	Val	Tyr	Glu	Thr	Asp	Tyr	Tyr	Arg	Lys
				1140					1145					1150	
Gly	Gly	Lys	Gly	Leu	Leu	Pro	Val	Arg	Trp	Met	Ala	Pro	Glu	Ser	Leu
				1155					1160					1165	
Lys	Asp	Gly	Ile	Phe	Thr	Thr	His	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val
				1170					1175					1180	
Val	Leu	Trp	Glu	Ile	Val	Thr	Leu	Ala	Glu	Gln	Pro	Tyr	Gln	Gly	Leu
1185					1190					1195					1200
Ser	Asn	Glu	Gln	Val	Leu	Lys	Phe	Val	Met	Asp	Gly	Gly	Val	Leu	Glu
				1205					1210					1215	
Glu	Leu	Glu	Gly	Cys	Pro	Leu	Gln	Leu	Gln	Glu	Leu	Met	Ser	Arg	Cys
				1220					1225					1230	
Trp	Gln	Pro	Asn	Pro	Arg	Leu	Arg	Pro	Ser	Phe	Thr	His	Ile	Leu	Asp
				1235					1240					1245	
Ser	Ile	Gln	Glu	Glu	Leu	Arg	Pro	Ser	Phe	Arg	Leu	Leu	Ser	Phe	Tyr
				1250					1255					1260	
Tyr	Ser	Pro	Glu	Cys	Arg	Gly	Ala	Arg	Gly	Ser	Leu	Pro	Thr	Thr	Asp
1265					1270					1275					1280
Ala	Glu	Pro	Asp	Ser	Ser	Pro	Thr	Pro	Arg	Asp	Cys	Ser	Pro	Gln	Asn
				1285					1290					1295	
Gly	Gly	Gly	Arg	Gly	Cys	Arg	Glu	Pro	Arg	Ser	His	His	Cys		
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Met	Asn	Val	Met	His	Val	Gly	Asn	Pro	Ser	Ala	Thr	Asp	Gln	Pro	Ser	
1				5					10					15		
ctg	tgc	atc	aga	gaa	cac	aca	cag	ggg	aga	aac	cat	aga	caa	cgg	aaa	96
Leu	Cys	Ile	Arg	Glu	His	Thr	Gln	Gly	Arg	Asn	His	Arg	Gln	Arg	Lys	
			20					25					30			
atg	tta	gca	aag	cgg	aaa	cct	cct	gcc	atg	ggg	cag	gac	cct	cct	gca	144
Met	Leu	Ala	Lys	Arg	Lys	Pro	Pro	Ala	Met	Gly	Gln	Asp	Pro	Pro	Ala	
		35					40					45				
acc	agt	gag	cag	aaa	cag	tgg	aaa	agc	agg	acc	aat	gga	gct	gaa	aat	192
Thr	Ser	Glu	Gln	Lys	Gln	Trp	Lys	Ser	Arg	Thr	Asn	Gly	Ala	Glu	Asn	
	50					55					60					

120/155

aaa acg tta aca tta gca gaa tac cat gaa caa gaa gaa atc ttc aaa	240
Lys Thr Leu Thr Leu Ala Glu Tyr His Glu Gln Glu Glu Ile Phe Lys	
65 70 75 80	
ctc cgg tta ggt cat ctt aaa aag gag gaa gca gag atc cag gca gag	288
Leu Arg Leu Gly His Leu Lys Lys Glu Glu Ala Glu Ile Gln Ala Glu	
85 90 95	
ctg gaa agg cta gaa agg gtt aga aat cta cgt atc ggg gaa cta aaa	336
Leu Glu Arg Leu Glu Arg Val Arg Asn Leu Arg Ile Gly Glu Leu Lys	
100 105 110	
agg ata cat aat gaa gat aac tca caa ttt aaa gat cat cca atg cta	384
Arg Ile His Asn Glu Asp Asn Ser Gln Phe Lys Asp His Pro Met Leu	
115 120 125	
aat gac aga tat ttg ttg tta cat ctt ttg gat aga gga ggt ttc agt	432
Asn Asp Arg Tyr Leu Leu Leu His Leu Leu Asp Arg Gly Gly Phe Ser	
130 135 140	
aaa gtt tac aag gca ttt gaa cta ata gag caa aga tac gta gct gtg	480
Lys Val Tyr Lys Ala Phe Glu Leu Ile Glu Gln Arg Tyr Val Ala Val	
145 150 155 160	
aaa att cac cag tta aat aaa aac tgg aga gat gag aaa aag gag aat	528
Lys Ile His Gln Leu Asn Lys Asn Trp Arg Asp Glu Lys Lys Glu Asn	
165 170 175	
tac cac aag cat gca tgt agg gaa tac tgg att cat aaa gaa ctg gat	576
Tyr His Lys His Ala Cys Arg Glu Tyr Trp Ile His Lys Glu Leu Asp	
180 185 190	
cat ccc aga ata att aag ctg tat gat tac ttt tca ctg gat act gac	624
His Pro Arg Ile Ile Lys Leu Tyr Asp Tyr Phe Ser Leu Asp Thr Asp	
195 200 205	
tca ttt tgt aca gtg tta gaa tac tgt gag gga aat gat cta aac ttc	672
Ser Phe Cys Thr Val Leu Glu Tyr Cys Glu Gly Asn Asp Leu Asn Phe	
210 215 220	
tat ctg aaa cgg cac aaa tta atg tca gag aaa gag gcc tgg tcc att	720
Tyr Leu Lys Arg His Lys Leu Met Ser Glu Lys Glu Ala Trp Ser Ile	
225 230 235 240	
atc atg cag act gta aat gct tta aag tac tta aat aaa ata aaa cct	768
Ile Met Gln Thr Val Asn Ala Leu Lys Tyr Leu Asn Lys Ile Lys Pro	
245 250 255	
ccc atc ata cac tat gac ctc aaa cca ggg aat att ctt tta gta aat	816
Pro Ile Ile His Tyr Asp Leu Lys Pro Gly Asn Ile Leu Leu Val Asn	
260 265 270	
ggt aca gtg tgt gga gag aga aaa att aca gag ctt ggt ctt tcg aag	864
Gly Thr Val Cys Gly Glu Arg Lys Ile Thr Glu Leu Gly Leu Ser Lys	
275 280 285	
atc atg gat gat gat agc tac aat tca gtg ggt ggc atg gag ctg aca	912
Ile Met Asp Asp Asp Ser Tyr Asn Ser Val Gly Gly Met Glu Leu Thr	
290 295 300	

121/155

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tca caa ggt gct ggc act tat tgc aat tta aca cca gag agt ttt gtg 960
Ser Gln Gly Ala Gly Thr Tyr Cys Asn Leu Thr Pro Glu Ser Phe Val
305 310 315 320

gtt gag aaa gaa cca cca aag atc tca aat aaa att gtt gtg tgg tcg 1008
Val Glu Lys Glu Pro Pro Lys Ile Ser Asn Lys Ile Val Val Trp Ser
325 330 335

gtg ggt gtg atc ttc tat cag tgt ctt tct gga ggg aag cct ttt ggc 1056
Val Gly Val Ile Phe Tyr Gln Cys Leu Ser Gly Gly Lys Pro Phe Gly
340 345 350

tat aac cag tct cag caa gac atc cta caa gag aat act att ctt aaa 1104
Tyr Asn Gln Ser Gln Gln Asp Ile Leu Gln Glu Asn Thr Ile Leu Lys
355 360 365

gct gct gaa gag gag tca gtc ttg ctt tct cag ggg tgg cag agg cag 1152
Ala Ala Glu Glu Glu Ser Val Leu Leu Ser Gln Gly Trp Gln Arg Gln
370 375 380

aag tgg agg aga tgg aag gga ggc agg aga ggc aaa cac acg tgg tat 1200
Lys Trp Arg Arg Trp Lys Gly Gly Arg Arg Gly Lys His Thr Trp Tyr
385 390 395 400

aac ttt cca gaa cta cat cat aat ttc tgt ctg atg ctt ttt gct ttt 1248
Asn Phe Pro Glu Leu His His Asn Phe Cys Leu Met Leu Phe Ala Phe
405 410 415

cta aaa agg tat ctg tac agt aac agt cct att gtt tgt ttt gat ttc 1296
Leu Lys Arg Tyr Leu Tyr Ser Asn Ser Pro Ile Val Cys Phe Asp Phe
420 425 430

agc acc tgt att ata aaa ggt ttt aat ttt gtt gat gtt caa ttt att 1344
Ser Thr Cys Ile Ile Lys Gly Phe Asn Phe Val Asp Val Gln Phe Ile
435 440 445

cat ttt ttc ttt ggg tcc ctg act tcc tgc aac aac ata tct ttt ctg 1392
His Phe Phe Phe Gly Ser Leu Thr Ser Cys Asn Asn Ile Ser Phe Leu
450 455 460

tct tct act ttt ttt cat tgg aac cca aca gaa tca aac tca aac att 1440
Ser Ser Thr Phe Phe His Trp Asn Pro Thr Glu Ser Asn Ser Asn Ile
465 470 475 480

aaa atc ctt act tta
Lys Ile Leu Thr Leu
485

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Leu Cys Ile Arg Glu His Thr Gln Gly Arg Asn His Arg Gln Arg Lys
20 25 30
Met Leu Ala Lys Arg Lys Pro Pro Ala Met Gly Gln Asp Pro Pro Ala
35 40 45

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122/155

Thr	Ser	Glu	Gln	Lys	Gln	Trp	Lys	Ser	Arg	Thr	Asn	Gly	Ala	Glu	Asn
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Lys	Thr	Leu	Thr	Leu	Ala	Glu	Tyr	His	Glu	Gln	Glu	Glu	Ile	Phe	Lys
65					70					75					80
Leu	Arg	Leu	Gly	His	Leu	Lys	Lys	Glu	Glu	Ala	Glu	Ile	Gln	Ala	Glu
			85					90						95	
Leu	Glu	Arg	Leu	Glu	Arg	Val	Arg	Asn	Leu	Arg	Ile	Gly	Glu	Leu	Lys
			100					105					110		
Arg	Ile	His	Asn	Glu	Asp	Asn	Ser	Gln	Phe	Lys	Asp	His	Pro	Met	Leu
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Asn	Asp	Arg	Tyr	Leu	Leu	Leu	His	Leu	Leu	Asp	Arg	Gly	Gly	Phe	Ser
	130					135					140				
Lys	Val	Tyr	Lys	Ala	Phe	Glu	Leu	Ile	Glu	Gln	Arg	Tyr	Val	Ala	Val
145					150					155					160
Lys	Ile	His	Gln	Leu	Asn	Lys	Asn	Trp	Arg	Asp	Glu	Lys	Lys	Glu	Asn
			165					170						175	
Tyr	His	Lys	His	Ala	Cys	Arg	Glu	Tyr	Trp	Ile	His	Lys	Glu	Leu	Asp
		180						185					190		
His	Pro	Arg	Ile	Ile	Lys	Leu	Tyr	Asp	Tyr	Phe	Ser	Leu	Asp	Thr	Asp
		195					200					205			
Ser	Phe	Cys	Thr	Val	Leu	Glu	Tyr	Cys	Glu	Gly	Asn	Asp	Leu	Asn	Phe
	210					215					220				
Tyr	Leu	Lys	Arg	His	Lys	Leu	Met	Ser	Glu	Lys	Glu	Ala	Trp	Ser	Ile
225					230					235					240
Ile	Met	Gln	Thr	Val	Asn	Ala	Leu	Lys	Tyr	Leu	Asn	Lys	Ile	Lys	Pro
			245						250					255	
Pro	Ile	Ile	His	Tyr	Asp	Leu	Lys	Pro	Gly	Asn	Ile	Leu	Leu	Val	Asn
			260					265					270		
Gly	Thr	Val	Cys	Gly	Glu	Arg	Lys	Ile	Thr	Glu	Leu	Gly	Leu	Ser	Lys
		275					280					285			
Ile	Met	Asp	Asp	Asp	Ser	Tyr	Asn	Ser	Val	Gly	Gly	Met	Glu	Leu	Thr
	290					295					300				
Ser	Gln	Gly	Ala	Gly	Thr	Tyr	Cys	Asn	Leu	Thr	Pro	Glu	Ser	Phe	Val
305					310					315					320
Val	Glu	Lys	Glu	Pro	Pro	Lys	Ile	Ser	Asn	Lys	Ile	Val	Val	Trp	Ser
			325						330					335	
Val	Gly	Val	Ile	Phe	Tyr	Gln	Cys	Leu	Ser	Gly	Gly	Lys	Pro	Phe	Gly
		340						345					350		
Tyr	Asn	Gln	Ser	Gln	Gln	Asp	Ile	Leu	Gln	Glu	Asn	Thr	Ile	Leu	Lys
		355				360						365			
Ala	Ala	Glu	Glu	Glu	Ser	Val	Leu	Leu	Ser	Gln	Gly	Trp	Gln	Arg	Gln
	370					375					380				
Lys	Trp	Arg	Arg	Trp	Lys	Gly	Gly	Arg	Arg	Gly	Lys	His	Thr	Trp	Tyr
385					390					395					400
Asn	Phe	Pro	Glu	Leu	His	His	Asn	Phe	Cys	Leu	Met	Leu	Phe	Ala	Phe
			405					410					415		
Leu	Lys	Arg	Tyr	Leu	Tyr	Ser	Asn	Ser	Pro	Ile	Val	Cys	Phe	Asp	Phe
			420				425					430			
Ser	Thr	Cys	Ile	Ile	Lys	Gly	Phe	Asn	Phe	Val	Asp	Val	Gln	Phe	Ile
		435					440					445			
His	Phe	Phe	Phe	Gly	Ser	Leu	Thr	Ser	Cys	Asn	Asn	Ile	Ser	Phe	Leu
	450					455					460				
Ser	Ser	Thr	Phe	Phe	His	Trp	Asn	Pro	Thr	Glu	Ser	Asn	Ser	Asn	Ile
465					470					475					480
Lys	Ile	Leu	Thr	Leu											
				485											

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<211> 1323

<212> DNA

<213> Homo sapiens

123/155

<220>

<221> CDS

<222> (1)...(1323)

<223> MOOSE08757

<400> 63

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ata aat aag aac gca aaa ata aaa aca cac acc cac agc cat ctg atc	96
Ile Asn Lys Asn Ala Lys Ile Lys Thr His Thr His Ser His Leu Ile	
20 25 30	
ttc aac caa gtc gac aaa agt aag caa tgg gga aag gac acc cta gta	144
Phe Asn Gln Val Asp Lys Ser Lys Gln Trp Gly Lys Asp Thr Leu Val	
35 40 45	
aat aaa tgg atg aca aac aac agc ggc tcc aaa gcc gaa ctc gtt gtg	192
Asn Lys Trp Met Thr Asn Asn Ser Gly Ser Lys Ala Glu Leu Val Val	
50 55 60	
gga ggg aaa tac aaa ctg gtg cgg aag atc ggg tct ggc tcc ttt gga	240
Gly Gly Lys Tyr Lys Leu Val Arg Lys Ile Gly Ser Gly Ser Phe Gly	
65 70 75 80	
gac gtt tat ctg ggc atc acc acc acc aac ggc gag gac gta gca gtg	288
Asp Val Tyr Leu Gly Ile Thr Thr Thr Asn Gly Glu Asp Val Ala Val	
85 90 95	
aag ctg gaa tct cag aag gtc aag cac ccc cag ttg ctg tat gag agc	336
Lys Leu Glu Ser Gln Lys Val Lys His Pro Gln Leu Leu Tyr Glu Ser	
100 105 110	
aaa ctc tac acg att ctt caa ggt ggg gtt ggc atc ccc cac atg cac	384
Lys Leu Tyr Thr Ile Leu Gln Gly Gly Val Gly Ile Pro His Met His	
115 120 125	
tgg tat ggt cag gaa aaa gac aac aat gtg cta gtc atg gac ctt ctg	432
Trp Tyr Gly Gln Glu Lys Asp Asn Asn Val Leu Val Met Asp Leu Leu	
130 135 140	
gga ccc agc ctc gaa gac ctc ttt aat ttc tgt tca aga agg ttc acc	480
Gly Pro Ser Leu Glu Asp Leu Phe Asn Phe Cys Ser Arg Arg Phe Thr	
145 150 155 160	
atg aaa act gta ctt atg tta gcc gac cag atg atc agc aga att gaa	528
Met Lys Thr Val Leu Met Leu Ala Asp Gln Met Ile Ser Arg Ile Glu	
165 170 175	
tac gtg cat aca aag aat ttt cta cac cga gac att aaa cca gat aac	576
Tyr Val His Thr Lys Asn Phe Leu His Arg Asp Ile Lys Pro Asp Asn	
180 185 190	
ttc ctg atg ggt act ggg cgt cac tgt aat aag ttg ttc ctt att gat	624
Phe Leu Met Gly Thr Gly Arg His Cys Asn Lys Leu Phe Leu Ile Asp	
195 200 205	
ttt ggt ttg gcc aaa aag tac aga gac aac agg acc agg caa cac ata	672
Phe Gly Leu Ala Lys Lys Tyr Arg Arg Asp Asn Arg Thr Arg Gln His Ile	
210 215 220	

124/155

ccg tac aga gaa gat aaa cac ctc att ggc act gtc cga tat gcc agc	720
Pro Tyr Arg Glu Asp Lys His Leu Ile Gly Thr Val Arg Tyr Ala Ser	
225 230 235 240	
atc aat gca cat ctt ggt att gag cag agc cgc cga gat gac atg gaa	768
Ile Asn Ala His Leu Gly Ile Glu Gln Ser Arg Arg Asp Asp Met Glu	
245 250 255	
tcc tta ggc tac gtt ttc atg tat ttt aat aga acc agc ctg ccg tgg	816
Ser Leu Gly Tyr Val Phe Met Tyr Phe Asn Arg Thr Ser Leu Pro Trp	
260 265 270	
caa gga cta agg gct atg aca aaa aaa caa aaa tat gaa aag att agt	864
Gln Gly Leu Arg Ala Met Thr Lys Lys Gln Lys Tyr Glu Lys Ile Ser	
275 280 285	
gag aag aag atg tcc acc cct gtt gaa gtt tta tgt aag ggg ttt cct	912
Glu Lys Lys Met Ser Thr Pro Val Glu Val Leu Cys Lys Gly Phe Pro	
290 295 300	
gca gaa ttc gcc atg tac ttg aac tac tgt cgt ggg ctg cgc ttt gag	960
Ala Glu Phe Ala Met Tyr Leu Asn Tyr Cys Arg Gly Leu Arg Phe Glu	
305 310 315 320	
gaa gtc cca gat tac atg tat ctg agg cag cta ttc cgc att ctt ttc	1008
Glu Val Pro Asp Tyr Met Tyr Leu Arg Gln Leu Phe Arg Ile Leu Phe	
325 330 335	
agg acc ctg aac cac caa tat gac tac aca ttt gat tgg acg atg tta	1056
Arg Thr Leu Asn His Gln Tyr Asp Tyr Thr Phe Asp Trp Thr Met Leu	
340 345 350	
aag cag aaa gca gca cag cag gca gcc tct tcc agt ggg cag ggt cag	1104
Lys Gln Lys Ala Ala Gln Gln Ala Ala Ser Ser Ser Gly Gln Gly Gln	
355 360 365	
cag gcc caa acc cag aca ggc aag caa act gaa aaa aac aag aat aat	1152
Gln Ala Gln Thr Gln Thr Gly Lys Gln Thr Glu Lys Asn Lys Asn Asn	
370 375 380	
ctt tgt aaa aca aaa tat agg tgt ttt tgt cct agt ata tca tta ttc	1200
Leu Cys Lys Thr Lys Tyr Arg Cys Phe Cys Pro Ser Ile Ser Leu Phe	
385 390 395 400	
cat ttt tct tct aga tac cat tca ttg tct tca cag ttc aca aaa gaa	1248
His Phe Ser Ser Arg Tyr His Ser Leu Ser Ser Gln Phe Thr Lys Glu	
405 410 415	
gaa tac aag cct ggg caa cat ggt gaa acc tca tct cta cta aaa aat	1296
Glu Tyr Lys Pro Gly Gln His Gly Glu Thr Ser Ser Leu Leu Lys Asn	
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aca aaa agt agc cag gca tgg tgg tgg	1323
Thr Lys Ser Ser Gln Ala Trp Trp Trp	
435 440	

<210> 64
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 <212> PRT
 <213> Homo sapiens

125/155

<400> 64

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Ile Asn Lys Asn Ala Lys Ile Lys Thr His Thr His Ser His Leu Ile
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Phe Asn Gln Val Asp Lys Ser Lys Gln Trp Gly Lys Asp Thr Leu Val
          35           40           45
Asn Lys Trp Met Thr Asn Asn Ser Gly Ser Lys Ala Glu Leu Val Val
          50           55           60
Gly Gly Lys Tyr Lys Leu Val Arg Lys Ile Gly Ser Gly Ser Phe Gly
65           70           75           80
Asp Val Tyr Leu Gly Ile Thr Thr Thr Asn Gly Glu Asp Val Ala Val
          85           90           95
Lys Leu Glu Ser Gln Lys Val Lys His Pro Gln Leu Leu Tyr Glu Ser
          100          105          110
Lys Leu Tyr Thr Ile Leu Gln Gly Gly Val Gly Ile Pro His Met His
          115          120          125
Trp Tyr Gly Gln Glu Lys Asp Asn Asn Val Leu Val Met Asp Leu Leu
          130          135          140
Gly Pro Ser Leu Glu Asp Leu Phe Asn Phe Cys Ser Arg Arg Phe Thr
145          150          155          160
Met Lys Thr Val Leu Met Leu Ala Asp Gln Met Ile Ser Arg Ile Glu
          165          170          175
Tyr Val His Thr Lys Asn Phe Leu His Arg Asp Ile Lys Pro Asp Asn
          180          185          190
Phe Leu Met Gly Thr Gly Arg His Cys Asn Lys Leu Phe Leu Ile Asp
          195          200          205
Phe Gly Leu Ala Lys Lys Tyr Arg Asp Asn Arg Thr Arg Gln His Ile
          210          215          220
Pro Tyr Arg Glu Asp Lys His Leu Ile Gly Thr Val Arg Tyr Ala Ser
225          230          235          240
Ile Asn Ala His Leu Gly Ile Glu Gln Ser Arg Arg Asp Asp Met Glu
          245          250          255
Ser Leu Gly Tyr Val Phe Met Tyr Phe Asn Arg Thr Ser Leu Pro Trp
          260          265          270
Gln Gly Leu Arg Ala Met Thr Lys Lys Gln Lys Tyr Glu Lys Ile Ser
          275          280          285
Glu Lys Lys Met Ser Thr Pro Val Glu Val Leu Cys Lys Gly Phe Pro
          290          295          300
Ala Glu Phe Ala Met Tyr Leu Asn Tyr Cys Arg Gly Leu Arg Phe Glu
305          310          315          320
Glu Val Pro Asp Tyr Met Tyr Leu Arg Gln Leu Phe Arg Ile Leu Phe
          325          330          335
Arg Thr Leu Asn His Gln Tyr Asp Tyr Thr Phe Asp Trp Thr Met Leu
          340          345          350
Lys Gln Lys Ala Ala Gln Gln Ala Ala Ser Ser Ser Gly Gln Gly Gln
          355          360          365
Gln Ala Gln Thr Gln Thr Gly Lys Gln Thr Glu Lys Asn Lys Asn Asn
          370          375          380
Leu Cys Lys Thr Lys Tyr Arg Cys Phe Cys Pro Ser Ile Ser Leu Phe
385          390          395          400
His Phe Ser Ser Arg Tyr His Ser Leu Ser Ser Gln Phe Thr Lys Glu
          405          410          415
Glu Tyr Lys Pro Gly Gln His Gly Glu Thr Ser Ser Leu Leu Lys Asn
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Thr Lys Ser Ser Gln Ala Trp Trp Trp
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<210> 65

<211> 1779

<212> DNA

126/155

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1779)

<223> MOOSE03397

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Val	Ala	Val	Ser	Arg	Asp	His	Ala	Thr	Ala	Leu	Gln	Pro	Gly	Arg	Gln	
1				5					10					15		
gcg	aga	ctc	cgt	ctc	aaa	aaa	aaa	aaa	aaa	aaa	aaa	aaa	gga	aag	aaa	96
Ala	Arg	Leu	Arg	Leu	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Gly	Lys	Lys	
			20					25					30			
gaa	aga	aag	aag	tca	gct	cag	gac	atg	tgt	caa	ttg	tac	ccc	gca	gcc	144
Glu	Arg	Lys	Lys	Ser	Ala	Gln	Asp	Met	Cys	Gln	Leu	Tyr	Pro	Ala	Ala	
		35					40					45				
cct	caa	gga	aac	cat	cat	tct	ggg	ttg	agt	cgc	ccc	ctg	gtc	gcc	gcc	192
Pro	Gln	Gly	Asn	His	His	Ser	Gly	Leu	Ser	Arg	Pro	Leu	Val	Ala	Ala	
	50					55					60					
ttc	ctg	cga	gac	ccg	ggc	tcg	ggc	cgc	gtg	tac	agg	cgc	ggg	aag	ctg	240
Phe	Leu	Arg	Asp	Pro	Gly	Ser	Gly	Arg	Val	Tyr	Arg	Arg	Gly	Lys	Leu	
65					70				75						80	
atc	ggc	aag	ggc	gcc	ttc	agc	cgc	tgc	tac	aag	ctg	aca	gac	atg	tcc	288
Ile	Gly	Lys	Gly	Ala	Phe	Ser	Arg	Cys	Tyr	Lys	Leu	Thr	Asp	Met	Ser	
				85				90						95		
acc	agc	gcc	gtg	ttc	gcc	ctc	aag	gtg	gtg	ccg	tgc	ggg	tac	atg	tcg	336
Thr	Ser	Ala	Val	Phe	Ala	Leu	Lys	Val	Val	Pro	Cys	Gly	Tyr	Met	Ser	
			100					105					110			
ggg	ccg	tgc	ctg	cag	gtg	gag	cgt	gag	att	gcc	ctg	cat	agc	cgc	ctg	384
Gly	Pro	Cys	Leu	Gln	Val	Glu	Arg	Glu	Ile	Ala	Leu	His	Ser	Arg	Leu	
		115					120					125				
cga	ccc	cgc	aac	atc	gtg	gct	ttc	cac	gga	cac	ttt	gct	gac	cgc	gac	432
Arg	Pro	Arg	Asn	Ile	Val	Ala	Phe	His	Gly	His	Phe	Ala	Asp	Arg	Asp	
	130					135					140					
cac	gtg	tac	atg	gtg	ctg	gag	tac	tgc	agc	cgc	cag	tct	ttg	gcc	cac	480
His	Val	Tyr	Met	Val	Leu	Glu	Tyr	Cys	Ser	Arg	Gln	Ser	Leu	Ala	His	
145					150				155						160	
gtg	ctg	agg	gcg	cgg	cag	atc	ctg	acg	gag	cca	gaa	gtg	cgc	gac	tac	528
Val	Leu	Arg	Ala	Arg	Gln	Ile	Leu	Thr	Glu	Pro	Glu	Val	Arg	Asp	Tyr	
				165				170						175		
ctg	cgg	ggc	ctg	gtc	agc	ggc	ctg	cgc	tac	ctg	cac	cag	cgg	tgc	atc	576
Leu	Arg	Gly	Leu	Val	Ser	Gly	Leu	Arg	Tyr	Leu	His	Gln	Arg	Cys	Ile	
			180					185					190			
ctg	cac	cgc	gac	ctg	aag	ctc	agt	aac	ttc	ttc	ctt	aac	aag	aac	atg	624
Leu	His	Arg	Asp	Leu	Lys	Leu	Ser	Asn	Phe	Phe	Leu	Asn	Lys	Asn	Met	
		195					200					205				

127/155

gag Glu	gtg Val	aag Lys	att Ile	gga Gly	gac Asp	ctg Leu	gga Gly	ctg Leu	gcg Ala	gcc Ala	aag Lys	gtg Val	ggg Gly	cca Pro	ggg Gly	672
210						215					220					
ggc Gly	cgc Arg	tgc Cys	cac His	aga Arg	gta Val	ctc Leu	tgt Cys	ggg Gly	acc Thr	cct Pro	aac Asn	ttc Phe	ctg Leu	gac Asp	cct Pro	720
225					230					235					240	
gag Glu	gtt Val	gtc Val	tcc Ser	aga Arg	aac Asn	ggt Gly	cac His	tcc Ser	tgc Cys	cag Gln	tac Tyr	acg Thr	gtg Val	ctg Leu	act Thr	768
				245					250					255		
ggc Gly	acc Thr	cca Pro	ccc Pro	ttc Phe	atg Met	gcc Ala	tca Ser	ccc Pro	ctg Leu	tcg Ser	gag Glu	atg Met	tac Tyr	caa Gln	aac Asn	816
			260					265					270			
atc Ile	cg Arg	gag Glu	ggc Gly	cac His	tac Tyr	ccc Pro	gaa Glu	ccc Pro	gct Ala	cac His	ctg Leu	tct Ser	gcc Ala	aat Asn	gcg Ala	864
		275					280					285				
cg Arg	cg Arg	ctc Leu	atc Ile	gtg Val	cac His	ctc Leu	cta Leu	gca Ala	ccc Pro	aac Asn	ccg Pro	gcc Ala	gag Glu	cg Arg	ccc Pro	912
290						295					300					
agc Ser	ctg Leu	gac Asp	cac His	ctg Leu	ctg Leu	cag Gln	gac Asp	gac Asp	ttc Phe	ttc Phe	aca Thr	cag Gln	ggg Gly	ttc Phe	act Thr	960
305					310				315						320	
cca Pro	gac Asp	cg Arg	ctg Leu	ccg Pro	gcc Ala	cac His	tcc Ser	tgc Cys	cac His	agt Ser	ccc Pro	ccc Pro	atc Ile	ttc Phe	gcc Ala	1008
				325					330					335		
ata Ile	ccc Pro	ccg Pro	cct Pro	ctg Leu	ggc Gly	agg Arg	atc Ile	ttc Phe	cg Arg	aag Lys	cct Pro	ggg Gly	gac Asp	aga Arg	gca Ala	1056
			340				345						350			
aga Arg	ctc Leu	tgt Cys	ctc Leu	aaa Lys	aaa Lys	aca Thr	aaa Lys	caa Gln	aac Asn	aaa Lys	aca Thr	aac Asn	aaa Lys	aac Asn	aca Thr	1104
		355				360					365					
cac His	acc Thr	cag Gln	aaa Lys	tgt Cys	gta Val	gta Val	ttt Phe	tca Ser	gag Glu	cat His	tgc Cys	aag Lys	tat Tyr	ttg Leu	aga Arg	1152
	370				375						380					
att Ile	gct Ala	cat His	tcc Ser	cag Gln	ggg Gly	tgc Cys	gcc Ala	agt Ser	atc Ile	cca Pro	cag Gln	tct Ser	ccc Pro	tct Ser	gca Ala	1200
385					390					395					400	
agc Ser	cag Gln	aaa Lys	tta Leu	cag Gln	cag Gln	ccc Pro	atc Ile	ctc Leu	tgg Trp	gcc Ala	ccc Pro	aaa Lys	tgg Trp	gtg Val	gat Asp	1248
				405					410					415		
tat Tyr	tcc Ser	agc Ser	aaa Lys	tac Tyr	ggc Gly	ttt Phe	ggc Gly	tac Tyr	cag Gln	ctc Leu	ttg Leu	gac Asp	ggg Gly	ggg Gly	ggc Gly	1296
			420				425						430			
gca Ala	cg Arg	gac Asp	ggc Gly	acc Thr	cac His	atg Met	gcc Ala	ctg Leu	cga Arg	ccc Pro	ccc Pro	gga Gly	ggc Gly	caa Gln	gtg Val	1344
		435					440					445				

128/155

tgc tac atg ccc aac tgc ggg agg ctg gaa gcc ttc gcc ctg agg gat Cys Tyr Met Pro Asn Cys Gly Arg Leu Glu Ala Phe Ala Leu Arg Asp 450 455 460	1392
gtg ccc ggc ctg ctg ggc gcc aag ctg gcc gtg ctg cag ctc ttt gcc Val Pro Gly Leu Leu Gly Ala Lys Leu Ala Val Leu Gln Leu Phe Ala 465 470 475 480	1440
ggc tgc ctg cgg cgg cgg ctg cgg gag gag ggg acc ctc ccc aca cct Gly Cys Leu Arg Arg Arg Leu Arg Glu Glu Gly Thr Leu Pro Thr Pro 485 490 495	1488
gtg cca cct gct gga ccc ggc ctc tgc ctc ctg cgc ttc ctg gcc tct Val Pro Pro Ala Gly Pro Gly Leu Cys Leu Leu Arg Phe Leu Ala Ser 500 505 510	1536
gag cac gcc ctg ctg ctg ctg ttc agc aat ggg atg gtg cag gtg agc Glu His Ala Leu Leu Leu Leu Phe Ser Asn Gly Met Val Gln Val Ser 515 520 525	1584
ttc agt gga gtc ccg gcc caa ctg gtg ctg agt ggc gag ggt gag ggt Phe Ser Gly Val Pro Ala Gln Leu Val Leu Ser Gly Glu Gly Glu Gly 530 535 540	1632
ttg cag ctc acc ctc tgg gag cag ggg tcc cct ggc acc tcc tac tcc Leu Gln Leu Thr Leu Trp Glu Gln Gly Ser Pro Gly Thr Ser Tyr Ser 545 550 555 560	1680
ctg gac gtc ccg cgg agc cac ggc tgc gcc ccc acc acc gga cag cac Leu Asp Val Pro Arg Ser His Gly Cys Ala Pro Thr Thr Gly Gln His 565 570 575	1728
ctt cac cac gcc ctc cgc atg ctg cag atg aga ctg aag aaa cca aag Leu His His Ala Leu Arg Met Leu Gln Met Arg Leu Lys Lys Pro Lys 580 585 590	1776
acc Thr	1779

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 <212> PRT
 <213> Homo sapiens

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 Glu Arg Lys Lys Ser Ala Gln Asp Met Cys Gln Leu Tyr Pro Ala Ala
 35 40 45
 Pro Gln Gly Asn His His Ser Gly Leu Ser Arg Pro Leu Val Ala Ala
 50 55 60
 Phe Leu Arg Asp Pro Gly Ser Gly Arg Val Tyr Arg Arg Gly Lys Leu
 65 70 75 80
 Ile Gly Lys Gly Ala Phe Ser Arg Cys Tyr Lys Leu Thr Asp Met Ser
 85 90 95
 Thr Ser Ala Val Phe Ala Leu Lys Val Val Pro Cys Gly Tyr Met Ser
 100 105 110

129/155

Gly 115	Pro 130	Cys 115	Leu 135	Gln 150	Val 165	Glu 180	Arg 120	Glu 135	Ile 155	Ala 170	Leu 185	His 125	Ser 140	Arg 155	Leu 160
Arg 145	Pro 160	Arg 130	Asn 150	Ile 165	Val 180	Ala 195	Phe 120	His 135	Gly 155	His 170	Phe 185	Ala 125	Asp 140	Arg 155	Asp 160
His 175	Val 190	Tyr 135	Met 150	Val 165	Leu 180	Glu 195	Tyr 120	Cys 135	Ser 155	Arg 170	Gln 185	Ser 125	Leu 140	Ala 155	His 160
Val 185	Leu 200	Arg 140	Ala 160	Arg 175	Gln 190	Ile 205	Leu 120	Thr 135	Glu 155	Pro 170	Glu 185	Val 125	Arg 140	Asp 155	Tyr 160
Leu 210	Arg 225	Gly 145	Leu 165	Val 180	Ser 195	Gly 205	Leu 120	Arg 135	Tyr 155	Leu 170	His 185	Gln 125	Arg 140	Cys 155	Ile 160
Leu 225	His 240	Arg 150	Asp 165	Leu 180	Lys 195	Leu 205	Ser 120	Asn 135	Phe 155	Phe 170	Leu 185	Asn 125	Lys 140	Asn 155	Met 160
Glu 240	Val 255	Lys 155	Ile 170	Gly 185	Asp 195	Leu 210	Gly 120	Leu 135	Ala 155	Ala 170	Lys 185	Val 125	Gly 140	Pro 155	Gly 160
Gly 255	Arg 270	Cys 160	His 175	Arg 190	Val 205	Leu 215	Cys 120	Gly 135	Thr 155	Pro 170	Asn 185	Phe 125	Leu 140	Asp 155	Pro 160
Glu 270	Val 285	Val 165	Ser 180	Arg 200	Asn 215	Gly 220	His 120	Ser 135	Cys 155	Gln 170	Tyr 185	Thr 125	Val 140	Leu 155	Thr 160
Gly 285	Thr 300	Pro 170	Pro 185	Phe 205	Met 215	Ala 225	Ser 120	Pro 135	Leu 155	Ser 170	Glu 185	Met 125	Tyr 140	Gln 155	Asn 160
Ile 300	Arg 315	Glu 175	Gly 190	His 205	Tyr 215	Pro 225	Glu 120	Pro 135	Ala 155	His 170	Leu 185	Ser 125	Ala 140	Asn 155	Ala 160
Arg 315	Arg 330	Leu 180	Ile 195	Val 205	His 215	Leu 225	Leu 120	Ala 135	Pro 155	Asn 170	Pro 185	Ala 125	Glu 140	Arg 155	Pro 160
Ser 330	Leu 345	Asp 185	His 195	Leu 205	Leu 215	Gln 225	Asp 120	Asp 135	Phe 155	Phe 170	Thr 185	Gln 125	Gly 140	Phe 155	Thr 160
Pro 345	Asp 360	Arg 190	Leu 200	Pro 210	Ala 220	His 230	Ser 120	Cys 135	His 155	Ser 170	Pro 185	Pro 125	Ile 140	Phe 155	Ala 160
Ile 360	Pro 375	Pro 195	Pro 205	Leu 215	Gly 225	Arg 235	Ile 120	Phe 135	Arg 155	Lys 170	Pro 185	Gly 125	Asp 140	Arg 155	Ala 160
Arg 375	Leu 390	Cys 200	Leu 210	Lys 220	Lys 230	Thr 240	Lys 120	Gln 135	Asn 155	Lys 170	Thr 185	Asn 125	Lys 140	Asn 155	Thr 160
His 390	Thr 405	Gln 205	Lys 215	Cys 225	Val 235	Val 245	Phe 120	Ser 135	Glu 155	His 170	Cys 185	Lys 125	Tyr 140	Leu 155	Arg 160
Ile 405	Ala 420	His 210	Ser 220	Gln 230	Gly 240	Cys 250	Ala 120	Ser 135	Ile 155	Pro 170	Gln 185	Ser 125	Pro 140	Ser 155	Ala 160
Ser 420	Gln 435	Lys 215	Leu 225	Gln 235	Gln 245	Pro 255	Ile 120	Leu 135	Trp 155	Ala 170	Pro 185	Lys 125	Trp 140	Val 155	Asp 160
Tyr 435	Ser 450	Ser 220	Lys 230	Tyr 240	Gly 250	Phe 260	Gly 120	Tyr 135	Gln 155	Leu 170	Leu 185	Asp 125	Gly 140	Gly 155	Gly 160
Ala 450	Arg 465	Asp 225	Gly 235	Thr 245	His 255	Met 265	Ala 120	Leu 135	Arg 155	Pro 170	Pro 185	Gly 125	Gly 140	Gln 155	Val 160
Cys 465	Tyr 480	Met 230	Pro 240	Asn 250	Cys 260	Gly 270	Arg 120	Glu 135	Leu 155	Ala 170	Phe 185	Ala 125	Leu 140	Arg 155	Asp 160
Val 480	Pro 495	Gly 235	Leu 245	Leu 255	Gly 265	Ala 275	Lys 120	Leu 135	Ala 155	Val 170	Leu 185	Gln 125	Leu 140	Phe 155	Ala 160
Gly 495	Cys 510	Leu 240	Arg 250	Arg 260	Arg 270	Leu 280	Arg 120	Glu 135	Glu 155	Gly 170	Thr 185	Leu 125	Pro 140	Thr 155	Pro 160
Val 510	Pro 525	Pro 245	Ala 255	Gly 265											

130/155

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 <211> 2307
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> MOOSE03609

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 ttg aat att ggc ccc cac tct ctt ctg gct tgt aga gtt tct gcg gag 96
 Leu Asn Ile Gly Pro His Ser Leu Leu Ala Cys Arg Val Ser Ala Glu
 20 25 30
 aga tca gct gtt agt ctg atg gca atg agc aag gct ccg tgg gca tgg 144
 Arg Ser Ala Val Ser Leu Met Ala Met Ser Lys Ala Pro Trp Ala Trp
 35 40 45
 cac cct cta agc cag tgg gat gcc atc act gaa atg gat gaa cat aat 192
 His Pro Leu Ser Gln Trp Asp Ala Ile Thr Glu Met Asp Glu His Asn
 50 55 60
 agg ccc att cac aca tac cag gta tgt aat gta atg gaa cca aac caa 240
 Arg Pro Ile His Thr Gln Val Cys Asn Val Met Glu Pro Asn Gln
 65 70 75 80
 aac aac tgg ctt cgt aca aac tgg atc tcc cgt gat gca gct cag aaa 288
 Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Arg Asp Ala Ala Gln Lys
 85 90 95
 att tat gtg gaa atg aaa ttc aca cta agg gat tgt aac agc atc cca 336
 Ile Tyr Val Glu Met Lys Phe Thr Leu Arg Asp Cys Asn Ser Ile Pro
 100 105 110
 tgg gtc ttg ggg act tgc aaa gaa aca ttt aat ctg ttt tat atg gaa 384
 Trp Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Phe Tyr Met Glu
 115 120 125
 tca gat gag tcc cac gga att aaa ttc aag cca aac cag tat aca aag 432
 Ser Asp Glu Ser His Gly Ile Lys Phe Lys Pro Asn Gln Tyr Thr Lys
 130 135 140
 atc gac aca att gct gct gat gag agt ttt acc cag atg gat ttg ggt 480
 Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Met Asp Leu Gly
 145 150 155 160
 gat cgc atc ctc aaa ctc aac act gaa att cgt gag gtg ggg cct ata 528
 Asp Arg Ile Leu Lys Leu Asn Thr Glu Ile Arg Glu Val Gly Pro Ile
 165 170 175
 gaa agg aaa gga ttt tat ctg gct ttt caa gac att ggg gcg tgc att 576
 Glu Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala Cys Ile
 180 185 190

131/155

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cgt	aac	ttg	gcc	atg	ttt	cct	gat	acc	att	cca	agg	gtt	gat	tcc	tcc	672
Arg	Asn	Leu	Ala	Met	Phe	Pro	Asp	Thr	Ile	Pro	Arg	Val	Asp	Ser	Ser	
	210					215					220					
tct	ttg	gtt	gaa	gta	cgg	ggg	tct	tgt	gtg	aag	agt	gct	gaa	gag	cgt	720
Ser	Leu	Val	Glu	Val	Arg	Gly	Ser	Cys	Val	Lys	Ser	Ala	Glu	Glu	Arg	
225					230					235					240	
gac	act	cct	aaa	ctg	tat	tgt	gga	gct	gat	gga	gat	tgg	ctg	gtt	cct	768
Asp	Thr	Pro	Lys	Leu	Tyr	Cys	Gly	Ala	Asp	Gly	Asp	Trp	Leu	Val	Pro	
				245					250					255		
ctt	gga	agg	tgc	atc	tgc	agt	aca	gga	tat	gaa	gaa	att	gag	ggg	tct	816
Leu	Gly	Arg	Cys	Ile	Cys	Ser	Thr	Gly	Tyr	Glu	Glu	Ile	Glu	Gly	Ser	
			260					265					270			
tgc	cat	gac	tgt	cat	att	gga	cat	ttt	gtg	ttt	aaa	att	tta	gac	ctg	864
Cys	His	Asp	Cys	His	Ile	Gly	His	Phe	Val	Phe	Lys	Ile	Leu	Asp	Leu	
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ctg	aga	atg	tgt	gtg	tgt	atg	tgt	gta	aat	ggg	ata	tac	agg	gcc	ttt	912
Leu	Arg	Met	Cys	Val	Cys	Met	Cys	Val	Asn	Gly	Ile	Tyr	Arg	Ala	Phe	
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aga	gat	cct	ttc	ccc	att	gct	tgt	ttt	tgt	cag	gtt	tgt	caa	gga	tca	960
Arg	Asp	Pro	Phe	Pro	Ile	Ala	Cys	Phe	Cys	Gln	Val	Cys	Gln	Gly	Ser	
305					310					315					320	
gat	ggg	tgt	aga	tgt	gtg	gtc	agt	atg	gcc	att	ttc	aca	tta	ttg	aat	1008
Asp	Gly	Cys	Arg	Cys	Val	Val	Ser	Met	Ala	Ile	Phe	Thr	Leu	Leu	Asn	
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ctt	cgt	atc	cat	gag	gat	gga	atg	ttt	tcc	cat	ttc	tct	tat	tat	ttt	1056
Leu	Arg	Ile	His	Glu	Asp	Gly	Met	Phe	Ser	His	Phe	Ser	Tyr	Tyr	Phe	
			340					345					350			
gag	atg	cat	tct	ggc	tgc	ata	ctg	cca	cag	cca	gta	ttt	tgg	gct	gtg	1104
Glu	Met	His	Ser	Gly	Cys	Ile	Leu	Pro	Gln	Pro	Val	Phe	Trp	Ala	Val	
		355					360					365				
ggg	aca	agt	ctt	ggg	acc	aaa	cca	tcc	agc	ctc	cct	ggc	tct	ggc	agg	1152
Gly	Thr	Ser	Leu	Gly	Thr	Lys	Pro	Ser	Ser	Leu	Pro	Gly	Ser	Gly	Arg	
	370					375					380					
gga	aaa	gag	cag	cct	aga	gct	ata	gaa	atg	ggg	gct	gcc	ctt	ccc	cca	1200
Gly	Lys	Glu	Gln	Pro	Arg	Ala	Ile	Glu	Met	Gly	Ala	Ala	Leu	Pro	Pro	
385					390					395					400	
tcc	agg	gag	ctt	agt	gtg	gta	ggc	agt	tgc	cag	att	tca	tat	tta	ttt	1248
Ser	Arg	Glu	Leu	Ser	Val	Val	Gly	Ser	Cys	Gln	Ile	Ser	Tyr	Leu	Phe	
				405					410					415		
gtc	ttc	gga	aag	aat	ttg	gtt	ttt	att	aaa	atg	cag	aaa	tat	ctg	aga	1296
Val	Phe	Gly	Lys	Asn	Leu	Val	Phe	Ile	Lys	Met	Gln	Lys	Tyr	Leu	Arg	
			420					425					430			

132/155

gag Glu	att Ile	gtt Val	agt Ser	aaa Lys	aaa Lys	tgt Cys	agg Arg	gat Asp	gtg Val	tat Tyr	gtg Val	gtg Val	cgt Arg	gtg Val	tgt Cys	1344
		435					440					445				
gtg Val	ttc Phe	aaa Lys	gat Asp	cac His	ggg Gly	tat Tyr	ggc Gly	aag Lys	gtt Val	agt Ser	ttc Phe	tgg Trp	tgg Trp	gga Gly	tgc Cys	1392
	450					455					460					
tct Ser	tcc Ser	tta Leu	ctt Leu	gca Ala	gaa Glu	gcc Ala	cac His	att Ile	ctt Leu	gct Ala	gtg Val	tca Ser	tca Ser	cat His	ggg Gly	1440
					470					475					480	
ttt Phe	tcc Ser	tct Ser	gtg Val	ctt Leu	gtg Val	cac His	ttg Leu	tct Ser	ctt Leu	ctt Leu	ctt Leu	atc Ile	agg Arg	aca Thr	aca Thr	1488
				485					490					495		
atc Ile	cta Leu	ttg Leu	tgt Cys	att Ile	gta Val	act Thr	cta Leu	cag Gln	gac Asp	atg Met	tct Ser	gac Asp	cct Pro	gtt Val	cac His	1536
			500					505					510			
tca Ser	tca Ser	cta Leu	aaa Lys	tta Leu	cta Leu	tat Tyr	aca Thr	acc Thr	aga Arg	att Ile	gtg Val	ctt Leu	gac Asp	aca Thr	tat Tyr	1584
		515					520					525				
aat Asn	gaa Glu	gca Ala	ttg Leu	aga Arg	aaa Lys	cat His	ttg Leu	agc Ser	tca Ser	ata Ile	aaa Lys	gtg Val	tct Ser	tcc Ser	ttt Phe	1632
	530					535					540					
ctt Leu	ttg Leu	tct Ser	tct Ser	tta Leu	ata Ile	ggg Gly	ggg Gly	atg Met	atc Ile	act Thr	atg Met	gat Asp	atc Ile	aaa Lys	atg Met	1680
	545				550					555					560	
gga Gly	agt Ser	tac Tyr	agt Ser	cat His	cct Pro	tat Tyr	tat Tyr	ata Ile	aga Arg	ata Ile	cag Gln	gga Gly	atc Ile	ctg Leu	agc Ser	1728
				565					570					575		
aag Lys	cgg Arg	tat Tyr	tat Tyr	gag Glu	gag Glu	gct Ala	gct Ala	gga Gly	gac Asp	tcg Ser	gta Val	ctc Leu	ttg Leu	gaa Glu	agg Arg	1776
		580						585					590			
ttc Phe	ata Ile	agc Ser	agt Ser	cta Leu	ctg Leu	aaa Lys	tgg Trp	tta Leu	tgt Cys	gca Ala	cac His	aca Thr	cac His	ata Ile	cac His	1824
		595					600					605				
ata Ile	cag Gln	agt Ser	act Thr	gtt Val	tct Ser	atg Met	ttc Phe	cag Gln	att Ile	gaa Glu	ttt Phe	ttt Phe	cct Pro	gaa Glu	aag Lys	1872
	610					615					620					
aag Lys	tac Tyr	aca Thr	agc Ser	act Thr	cca Pro	gca Ala	att Ile	tcc Ser	act Thr	ata Ile	aaa Lys	ttt Phe	ccc Pro	ttt Phe	tgg Trp	1920
	625				630					635					640	
ggc Gly	atg Met	aaa Lys	aat Asn	aat Asn	gtt Val	tgc Cys	aga Arg	agc Ser	att Ile	gaa Glu	tgt Cys	tgg Trp	gta Val	aga Arg	gga Gly	1968
				645					650					655		
gaa Glu	agt Ser	ggc Gly	agg Arg	aaa Lys	aca Thr	aga Arg	agg Arg	cct Pro	aag Lys	act Thr	caa Gln	cat His	ata Ile	aag Lys	gaa Glu	2016
			660					665					670			

133/155

gtt aat aaa gga gag aaa atg ata gcc cct cct cca aca cta caa att	2064
Val Asn Lys Gly Glu Lys Met Ile Ala Pro Pro Pro Thr Leu Gln Ile	
675 680 685	
aca att caa cat aag att tgg gta ggg aca caa atc caa acc atg tca	2112
Thr Ile Gln His Lys Ile Trp Val Gly Thr Gln Ile Gln Thr Met Ser	
690 695 700	
gta cct gat acc tca atc tat aga gat gtt tcc cag tct ttt gaa tat	2160
Val Pro Asp Thr Ser Ile Tyr Arg Asp Val Ser Gln Ser Phe Glu Tyr	
705 710 715 720	
att gtc ata caa aga aat ata tct gaa ttt gtc cac act ggt tgg aaa	2208
Ile Val Ile Gln Arg Asn Ile Ser Glu Phe Val His Thr Gly Trp Lys	
725 730 735	
tcc caa ata tat gca gaa cta aaa tgt tta gca ggg cac tca tgt aga	2256
Ser Gln Ile Tyr Ala Glu Leu Lys Cys Leu Ala Gly His Ser Cys Arg	
740 745 750	
gtt tta tcc ttc ata cat gta cag atg atg ctt tcc aaa cct aga ata	2304
Val Leu Ser Phe Ile His Val Gln Met Met Leu Ser Lys Pro Arg Ile	
755 760 765	
cct	2307
Pro	

<210> 68

<211> 769

<212> PRT

<213> Homo sapiens

<400> 68

Leu Ala Gly Tyr Glu Ile Leu Gly Cys Lys Phe Phe Ser Phe Arg Met	
1 5 10 15	
Leu Asn Ile Gly Pro His Ser Leu Leu Ala Cys Arg Val Ser Ala Glu	
20 25 30	
Arg Ser Ala Val Ser Leu Met Ala Met Ser Lys Ala Pro Trp Ala Trp	
35 40 45	
His Pro Leu Ser Gln Trp Asp Ala Ile Thr Glu Met Asp Glu His Asn	
50 55 60	
Arg Pro Ile His Thr Tyr Gln Val Cys Asn Val Met Glu Pro Asn Gln	
65 70 75 80	
Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Arg Asp Ala Ala Gln Lys	
85 90 95	
Ile Tyr Val Glu Met Lys Phe Thr Leu Arg Asp Cys Asn Ser Ile Pro	
100 105 110	
Trp Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Phe Tyr Met Glu	
115 120 125	
Ser Asp Glu Ser His Gly Ile Lys Phe Lys Pro Asn Gln Tyr Thr Lys	
130 135 140	
Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Met Asp Leu Gly	
145 150 155 160	
Asp Arg Ile Leu Lys Leu Asn Thr Glu Ile Arg Glu Val Gly Pro Ile	
165 170 175	
Glu Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala Cys Ile	
180 185 190	
Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Phe Thr Val	
195 200 205	

134/155

Arg	Asn	Leu	Ala	Met	Phe	Pro	Asp	Thr	Ile	Pro	Arg	Val	Asp	Ser	Ser
	210					215					220				
Ser	Leu	Val	Glu	Val	Arg	Gly	Ser	Cys	Val	Lys	Ser	Ala	Glu	Glu	Arg
225					230					235					240
Asp	Thr	Pro	Lys	Leu	Tyr	Cys	Gly	Ala	Asp	Gly	Asp	Trp	Leu	Val	Pro
				245					250					255	
Leu	Gly	Arg	Cys	Ile	Cys	Ser	Thr	Gly	Tyr	Glu	Glu	Ile	Glu	Gly	Ser
			260					265					270		
Cys	His	Asp	Cys	His	Ile	Gly	His	Phe	Val	Phe	Lys	Ile	Leu	Asp	Leu
		275					280					285			
Leu	Arg	Met	Cys	Val	Cys	Met	Cys	Val	Asn	Gly	Ile	Tyr	Arg	Ala	Phe
	290					295					300				
Arg	Asp	Pro	Phe	Pro	Ile	Ala	Cys	Phe	Cys	Gln	Val	Cys	Gln	Gly	Ser
305					310					315					320
Asp	Gly	Cys	Arg	Cys	Val	Val	Ser	Met	Ala	Ile	Phe	Thr	Leu	Leu	Asn
				325					330					335	
Leu	Arg	Ile	His	Glu	Asp	Gly	Met	Phe	Ser	His	Phe	Ser	Tyr	Tyr	Phe
			340					345					350		
Glu	Met	His	Ser	Gly	Cys	Ile	Leu	Pro	Gln	Pro	Val	Phe	Trp	Ala	Val
		355					360					365			
Gly	Thr	Ser	Leu	Gly	Thr	Lys	Pro	Ser	Ser	Leu	Pro	Gly	Ser	Gly	Arg
	370					375					380				
Gly	Lys	Glu	Gln	Pro	Arg	Ala	Ile	Glu	Met	Gly	Ala	Ala	Leu	Pro	Pro
385					390					395					400
Ser	Arg	Glu	Leu	Ser	Val	Val	Gly	Ser	Cys	Gln	Ile	Ser	Tyr	Leu	Phe
				405					410					415	
Val	Phe	Gly	Lys	Asn	Leu	Val	Phe	Ile	Lys	Met	Gln	Lys	Tyr	Leu	Arg
			420					425					430		
Glu	Ile	Val	Ser	Lys	Lys	Cys	Arg	Asp	Val	Tyr	Val	Val	Arg	Val	Cys
		435					440					445			
Val	Phe	Lys	Asp	His	Gly	Tyr	Gly	Lys	Val	Ser	Phe	Trp	Trp	Gly	Cys
	450					455					460				
Ser	Ser	Leu	Leu	Ala	Glu	Ala	His	Ile	Leu	Ala	Val	Ser	Ser	His	Gly
465					470					475					480
Phe	Ser	Ser	Val	Leu	Val	His	Leu	Ser	Leu	Leu	Leu	Ile	Arg	Thr	Thr
				485					490					495	
Ile	Leu	Leu	Cys	Ile	Val	Thr	Leu	Gln	Asp	Met	Ser	Asp	Pro	Val	His
			500					505					510		
Ser	Ser	Leu	Lys	Leu	Leu	Tyr	Thr	Thr	Arg	Ile	Val	Leu	Asp	Thr	Tyr
		515					520					525			
Asn	Glu	Ala	Leu	Arg	Lys	His	Leu	Ser	Ser	Ile	Lys	Val	Ser	Ser	Phe
	530					535					540				
Leu	Leu	Ser	Ser	Leu	Ile	Gly	Gly	Met	Ile	Thr	Met	Asp	Ile	Lys	Met
545					550					555					560
Gly	Ser	Tyr	Ser	His	Pro	Tyr	Tyr	Ile	Arg	Ile	Gln	Gly	Ile	Leu	Ser
				565					570					575	
Lys	Arg	Tyr	Tyr	Glu	Glu	Ala	Ala	Gly	Asp	Ser	Val	Leu	Leu	Glu	Arg
			580					585					590		
Phe	Ile	Ser	Ser	Leu	Leu	Lys	Trp	Leu	Cys	Ala	His	Thr	His	Ile	His
		595					600					605			
Ile	Gln	Ser	Thr	Val	Ser	Met	Phe	Gln	Ile	Glu	Phe	Phe	Pro	Glu	Lys
	610					615					620				
Lys	Tyr	Thr	Ser	Thr	Pro	Ala	Ile	Ser	Thr	Ile	Lys	Phe	Pro	Phe	Trp
625					630					635					640
Gly	Met	Lys	Asn	Asn	Val	Cys	Arg	Ser	Ile	Glu	Cys	Trp	Val	Arg	Gly
			645						650					655	
Glu	Ser	Gly	Arg	Lys	Thr	Arg	Arg	Pro	Lys	Thr	Gln	His	Ile	Lys	Glu
			660					665					670		
Val	Asn	Lys	Gly	Glu	Lys	Met	Ile	Ala	Pro	Pro	Pro	Thr	Leu	Gln	Ile
		675					680					685			
Thr	Ile	Gln	His	Lys	Ile	Trp	Val	Gly	Thr	Gln	Ile	Gln	Thr	Met	Ser
	690					695					700				

135/155

Val Pro Asp Thr Ser Ile Tyr Arg Asp Val Ser Gln Ser Phe Glu Tyr
 705 710 715 720
 Ile Val Ile Gln Arg Asn Ile Ser Glu Phe Val His Thr Gly Trp Lys
 725 730 735
 Ser Gln Ile Tyr Ala Glu Leu Lys Cys Leu Ala Gly His Ser Cys Arg
 740 745 750
 Val Leu Ser Phe Ile His Val Gln Met Met Leu Ser Lys Pro Arg Ile
 755 760 765
 Pro

<210> 69
 <211> 888
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (888)
 <223> MOOSE03184

<400> 69
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 Ala Ser Ser Tyr Leu Asn Leu Glu Lys Leu Gly Glu Gly Ser Tyr Ala
 1 5 10 15
 aca gtt tac aag ggg att agc aga ata aat gga caa cta gtg gct tta 96
 Thr Val Tyr Lys Gly Ile Ser Arg Ile Asn Gly Gln Leu Val Ala Leu
 20 25 30
 aaa gtc atc agc atg aat gca gag gaa gga gtc cca ttt aca gct atc 144
 Lys Val Ile Ser Met Asn Ala Glu Glu Gly Val Pro Phe Thr Ala Ile
 35 40 45
 cga gaa gct tct ctc ctg aag ggt ttg aaa cat gcc aat att gtg ctc 192
 Arg Glu Ala Ser Leu Leu Lys Gly Leu Lys His Ala Asn Ile Val Leu
 50 55 60
 ctg cat gac ata atc cac acc aaa gag aca ctg aca ttc gtt ttt gaa 240
 Leu His Asp Ile Ile His Thr Lys Glu Thr Leu Thr Phe Val Phe Glu
 65 70 75 80
 tac atg gtg agt tac ctg gcc cag tat atg tct cag cat cca gga ggg 288
 Tyr Met Val Ser Tyr Leu Ala Gln Tyr Met Ser Gln His Pro Gly Gly
 85 90 95
 ctt cat cct cat aat gtc aga ctt ttc atg ttt caa ctt ttg cgg ggc 336
 Leu His Pro His Asn Val Arg Leu Phe Met Phe Gln Leu Leu Arg Gly
 100 105 110
 ctg gcg tac atc cac cac caa cac gtt ctt cac agg gac ctg aaa cct 384
 Leu Ala Tyr Ile His His Gln His Val Leu His Arg Asp Leu Lys Pro
 115 120 125
 cag aac tta ctc atc agt cac ctg gga gag ctc aaa ctg gct gat ttt 432
 Gln Asn Leu Leu Ile Ser His Leu Gly Glu Leu Lys Leu Ala Asp Phe
 130 135 140
 ggt ctt gcc cgg gcc aag tcc att ccc agc cag aca tac tct tca gaa 480
 Gly Leu Ala Arg Ala Lys Ser Ile Pro Ser Gln Thr Tyr Ser Ser Glu
 145 150 155 160

136/155

gtc	gtg	acc	ctc	tgg	tac	cgg	ccc	cct	gat	gct	ttg	ctg	gga	gcc	act	528
Val	Val	Thr	Leu	Trp	Tyr	Arg	Pro	Pro	Asp	Ala	Leu	Leu	Gly	Ala	Thr	
				165					170					175		
gaa	tat	tcc	tct	gag	ctg	gac	ata	tgg	ggg	gca	ggc	tgc	atc	ttt	att	576
Glu	Tyr	Ser	Ser	Glu	Leu	Asp	Ile	Trp	Gly	Ala	Gly	Cys	Ile	Phe	Ile	
			180					185					190			
gaa	atg	ttc	cag	ggg	caa	cct	ttg	ttt	cct	ggg	gtt	tcc	aac	atc	ctt	624
Glu	Met	Phe	Gln	Gly	Gln	Pro	Leu	Phe	Pro	Gly	Val	Ser	Asn	Ile	Leu	
		195					200					205				
gaa	cag	ctg	gag	aaa	atc	tgg	gag	gtg	ctg	gga	gtc	cct	aca	gag	gat	672
Glu	Gln	Leu	Glu	Lys	Ile	Trp	Glu	Val	Leu	Gly	Val	Pro	Thr	Glu	Asp	
	210					215					220					
act	tgg	ccg	gga	gtc	tcc	aag	cta	cct	aac	tac	aat	cca	ggc	tgc	tgg	720
Thr	Trp	Pro	Gly	Val	Ser	Lys	Leu	Pro	Asn	Tyr	Asn	Pro	Gly	Cys	Trp	
225					230				235						240	
aga	aac	tct	att	ttt	ctc	tcc	cac	ttt	tcc	agg	ctg	ggc	agg	gtt	cct	768
Arg	Asn	Ser	Ile	Phe	Leu	Ser	His	Phe	Ser	Arg	Leu	Gly	Arg	Val	Pro	
				245					250					255		
gaa	gct	gaa	gac	ctg	gcc	tcc	cag	atg	cta	aaa	ggc	ttt	ccc	aga	gac	816
Glu	Ala	Glu	Asp	Leu	Ala	Ser	Gln	Met	Leu	Lys	Gly	Phe	Pro	Arg	Asp	
			260					265					270			
cgc	gtc	tcc	gcc	cag	gaa	gca	ctt	gtt	cat	gat	tat	ttc	agc	gcc	ctg	864
Arg	Val	Ser	Ala	Gln	Glu	Ala	Leu	Val	His	Asp	Tyr	Phe	Ser	Ala	Leu	
		275					280					285				
cca	tct	cag	ctg	tac	cag	ctt	cct									888
Pro	Ser	Gln	Leu	Tyr	Gln	Leu	Pro									
		290				295										

<210> 70
 <211> 296
 <212> PRT
 <213> Homo sapiens

<400> 70
 Ala Ser Ser Tyr Leu Asn Leu Glu Lys Leu Gly Glu Gly Ser Tyr Ala
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 Thr Val Tyr Lys Gly Ile Ser Arg Ile Asn Gly Gln Leu Val Ala Leu
 20 25 30
 Lys Val Ile Ser Met Asn Ala Glu Glu Gly Val Pro Phe Thr Ala Ile
 35 40 45
 Arg Glu Ala Ser Leu Leu Lys Gly Leu Lys His Ala Asn Ile Val Leu
 50 55 60
 Leu His Asp Ile Ile His Thr Lys Glu Thr Leu Thr Phe Val Phe Glu
 65 70 75 80
 Tyr Met Val Ser Tyr Leu Ala Gln Tyr Met Ser Gln His Pro Gly Gly
 85 90 95
 Leu His Pro His Asn Val Arg Leu Phe Met Phe Gln Leu Leu Arg Gly
 100 105 110
 Leu Ala Tyr Ile His His Gln His Val Leu His Arg Asp Leu Lys Pro
 115 120 125
 Gln Asn Leu Leu Ile Ser His Leu Gly Glu Leu Lys Leu Ala Asp Phe
 130 135 140

137/155

Gly Leu Ala Arg Ala Lys Ser Ile Pro Ser Gln Thr Tyr Ser Ser Glu
 145 150 155 160
 Val Val Thr Leu Trp Tyr Arg Pro Pro Asp Ala Leu Leu Gly Ala Thr
 165 170 175
 Glu Tyr Ser Ser Glu Leu Asp Ile Trp Gly Ala Gly Cys Ile Phe Ile
 180 185 190
 Glu Met Phe Gln Gly Gln Pro Leu Phe Pro Gly Val Ser Asn Ile Leu
 195 200 205
 Glu Gln Leu Glu Lys Ile Trp Glu Val Leu Gly Val Pro Thr Glu Asp
 210 215 220
 Thr Trp Pro Gly Val Ser Lys Leu Pro Asn Tyr Asn Pro Gly Cys Trp
 225 230 235 240
 Arg Asn Ser Ile Phe Leu Ser His Phe Ser Arg Leu Gly Arg Val Pro
 245 250 255
 Glu Ala Glu Asp Leu Ala Ser Gln Met Leu Lys Gly Phe Pro Arg Asp
 260 265 270
 Arg Val Ser Ala Gln Glu Ala Leu Val His Asp Tyr Phe Ser Ala Leu
 275 280 285
 Pro Ser Gln Leu Tyr Gln Leu Pro
 290 295

<210> 71
 <211> 1098
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (1098)
 <223> MOOSE03305

<400> 71
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 Ile Ala Ala Asn Val Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly
 1 5 10 15
 gat ggg aac ttt gct gtc gtg aag gag tgc aga cac cgc gag acc agg 96
 Asp Gly Asn Phe Ala Val Val Lys Glu Cys Arg His Arg Glu Thr Arg
 20 25 30
 cag gcc tat gcg atg aag atc att gac aag tcc aga ctc aag ggc aag 144
 Gln Ala Tyr Ala Met Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys
 35 40 45
 gag gac atg gtg gac agt gag atc ttg atc atc cag agc ctc tct cac 192
 Glu Asp Met Val Asp Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His
 50 55 60
 ccc aac atc gtg aaa ttg cat gaa gtc tac gaa aca gac atg gaa atc 240
 Pro Asn Ile Val Lys Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile
 65 70 75 80
 tac ctg atc ctg gag tac gtg cag gga gga gac ctt ttt gac gcc atc 288
 Tyr Leu Ile Leu Glu Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile
 85 90 95
 ata gaa agt gtg aag ttc ccg gag ccc gat gct gcc ctc atg atc atg 336
 Ile Glu Ser Val Lys Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met
 100 105 110

138/155

gac Asp	tta Leu	tgc Cys	aaa Lys	gcc Ala	ctc Leu	gtc Val	cac His	atg Met	cac His	gac Asp	aag Lys	agc Ser	att Ile	gtc Val	cac His	384
		115					120					125				
cgg Arg	gac Asp	ctc Leu	aag Lys	ccg Pro	gaa Glu	aac Asn	ctt Leu	ttg Leu	cga Arg	aat Asn	gag Glu	gac Asp	aaa Lys	tct Ser	act Thr	432
	130					135					140					
acc Thr	ttg Leu	aaa Lys	ttg Leu	gct Ala	gat Asp	ttt Phe	gga Gly	ctt Leu	gca Ala	aag Lys	cat His	gtg Val	gtg Val	aga Arg	cct Pro	480
	145				150					155					160	
ata Ile	ttt Phe	act Thr	gtg Val	tgt Cys	ggg Gly	acc Thr	cca Pro	act Thr	tac Tyr	gta Val	gct Ala	ccc Pro	gaa Glu	att Ile	ctt Leu	528
				165					170					175		
tct Ser	gag Glu	aaa Lys	ggt Gly	tat Tyr	gga Gly	ctg Leu	gag Glu	gtg Val	gac Asp	atg Met	tgg Trp	gct Ala	gct Ala	ggc Gly	gtg Val	576
			180					185					190			
atc Ile	ctc Leu	tat Tyr	atc Ile	ctg Leu	ctg Leu	tgt Cys	ggc Gly	ttt Phe	ccc Pro	cca Pro	ttc Phe	cgc Arg	agc Ser	cct Pro	gag Glu	624
		195					200					205				
agg Arg	gac Asp	cag Gln	gac Asp	gag Glu	ctc Leu	ttt Phe	aac Asn	atc Ile	atc Ile	cag Gln	ctg Leu	ggc Gly	cac His	ttt Phe	gag Glu	672
	210					215					220					
ttc Phe	ctc Leu	ccc Pro	cct Pro	tac Tyr	tgg Trp	gac Asp	aat Asn	atc Ile	tct Ser	gat Asp	gct Ala	gct Ala	aaa Lys	gat Asp	ctg Leu	720
	225				230					235					240	
gtg Val	agc Ser	cgg Arg	ttg Leu	ctg Leu	gtg Val	gta Val	gac Asp	ccc Pro	aaa Lys	aag Lys	cgc Arg	tac Tyr	aca Thr	gct Ala	cat His	768
				245					250					255		
cag Gln	gtt Val	ctt Leu	cag Gln	cac His	ccc Pro	tgg Trp	atc Ile	gaa Glu	aca Thr	gct Ala	ggc Gly	aag Lys	acc Thr	aat Asn	aca Thr	816
			260					265					270			
gtg Val	aaa Lys	cga Arg	cag Gln	aag Lys	cag Gln	gtg Val	tcc Ser	ccc Pro	agc Ser	agc Ser	gag Glu	ggt Gly	cac His	ttc Phe	cgg Arg	864
		275					280					285				
agc Ser	cag Gln	cac His	aag Lys	agg Arg	gtt Val	gtg Val	gag Glu	cag Gln	gta Val	tca Ser	tat Tyr	gaa Glu	tct Ser	ata Ile	gtg Val	912
		290				295					300					
aca Thr	gaa Glu	agt Ser	gat Asp	cag Gln	ggg Gly	gtt Val	tgc Cys	tgg Trp	aga Arg	tgg Trp	aaa Lys	tgg Trp	gga Gly	gag Glu	gag Glu	960
	305				310					315					320	
gga Gly	cag Gln	aag Lys	gat Asp	tgc Cys	aag Lys	gga Gly	aca Thr	ctt Leu	ggt Gly	aac Asn	ttt Phe	ggg Gly	gaa Glu	gag Glu	gga Gly	1008
				325					330					335		
cgt Arg	gtt Val	cat His	ttt Phe	ctt Leu	gaa Glu	ttg Leu	tgg Trp	aga Arg	aga Arg	aat Asn	ggg Gly	gaa Glu	atg Met	agt Ser	cca Pro	1056
			340					345					350			

139/155

gga aga gag gaa ggc caa gaa aga gtg cat tca cgt gtg agg
 Gly Arg Glu Glu Gly Gln Glu Arg Val His Ser Arg Val Arg
 355 360 365

1098

<210> 72
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 72
 Ile Ala Ala Asn Val Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly
 1 5 10 15
 Asp Gly Asn Phe Ala Val Val Lys Glu Cys Arg His Arg Glu Thr Arg
 20 25 30
 Gln Ala Tyr Ala Met Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys
 35 40 45
 Glu Asp Met Val Asp Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His
 50 55 60
 Pro Asn Ile Val Lys Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile
 65 70 75 80
 Tyr Leu Ile Leu Glu Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile
 85 90 95
 Ile Glu Ser Val Lys Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met
 100 105 110
 Asp Leu Cys Lys Ala Leu Val His Met His Asp Lys Ser Ile Val His
 115 120 125
 Arg Asp Leu Lys Pro Glu Asn Leu Leu Arg Asn Glu Asp Lys Ser Thr
 130 135 140
 Thr Leu Lys Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro
 145 150 155 160
 Ile Phe Thr Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu
 165 170 175
 Ser Glu Lys Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val
 180 185 190
 Ile Leu Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu
 195 200 205
 Arg Asp Gln Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu
 210 215 220
 Phe Leu Pro Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu
 225 230 235 240
 Val Ser Arg Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His
 245 250 255
 Gln Val Leu Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr
 260 265 270
 Val Lys Arg Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg
 275 280 285
 Ser Gln His Lys Arg Val Val Glu Gln Val Ser Tyr Glu Ser Ile Val
 290 295 300
 Thr Glu Ser Asp Gln Gly Val Cys Trp Arg Trp Lys Trp Gly Glu Glu
 305 310 315 320
 Gly Gln Lys Asp Cys Lys Gly Thr Leu Gly Asn Phe Gly Glu Glu Gly
 325 330 335
 Arg Val His Phe Leu Glu Leu Trp Arg Arg Asn Gly Glu Met Ser Pro
 340 345 350
 Gly Arg Glu Glu Gly Gln Glu Arg Val His Ser Arg Val Arg
 355 360 365

<210> 73
 <211> 1407

140/155

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1407)

<223> MOOSE03302

<400> 73

aaa ggt gtt gga aga ttt aaa gat cgg aaa tat gaa ata atc cga ttt	48
Lys Gly Val Gly Arg Phe Lys Asp Arg Lys Tyr Glu Ile Ile Arg Phe	
1 5 10 15	
cat tat aca aag ctc tct ctt gct gca gtg tgg caa ggg att ata gga	96
His Tyr Thr Lys Leu Ser Leu Ala Ala Val Trp Gln Gly Ile Ile Gly	
20 25 30	
ggg cag aat gga agt gga gga aaa tgg ata ttg gag gag tca aag aaa	144
Gly Gln Asn Gly Ser Gly Gly Lys Trp Ile Leu Glu Glu Ser Lys Lys	
35 40 45	
aaa aat gac aat gat ttg ggc ata ggt gag agc agt aga gga gaa aac	192
Lys Asn Asp Asn Asp Leu Gly Ile Gly Glu Ser Ser Arg Gly Glu Asn	
50 55 60	
tta tgt ttc atc ttc aaa agc tca gta aga gtg tgc cac gtt atg gag	240
Leu Cys Phe Ile Phe Lys Ser Ser Val Arg Val Cys His Val Met Glu	
65 70 75 80	
gtc cat gca tat acg ggg tct cac tat gtt gcc cag act gaa ttc ctg	288
Val His Ala Tyr Thr Gly Ser His Tyr Val Ala Gln Thr Glu Phe Leu	
85 90 95	
ggc tca agt gat cct cct gcc ttg gcc tcc caa aat gct gag gtt aca	336
Gly Ser Ser Asp Pro Pro Ala Leu Ala Ser Gln Asn Ala Glu Val Thr	
100 105 110	
agc ctg agc cac cac acc tat ctt gta agt ccc tgt agt aat aaa ata	384
Ser Leu Ser His His Thr Tyr Leu Val Ser Pro Cys Ser Asn Lys Ile	
115 120 125	
tat cct gaa tat ttt act gga ggt gaa ctg ttt gaa gac ata gtg gca	432
Tyr Pro Glu Tyr Phe Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala	
130 135 140	
aga gaa tac tac agt gaa gct gat gcc agt cat tgc att cag cag atc	480
Arg Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys Ile Gln Gln Ile	
145 150 155 160	
ctg gag gct gtg cta cac tgc cat cag atg ggc gtg gtc cat cgg gac	528
Leu Glu Ala Val Leu His Cys His Gln Met Gly Val Val His Arg Asp	
165 170 175	
ctg aag cct gag aat ttg ctt tta gct agc aaa tcc aag gga gca gct	576
Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Ser Lys Gly Ala Ala	
180 185 190	
gtg aaa ttg gca gac ttt ggc tta gcc ata gaa gtt caa ggg gac cag	624
Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Asp Gln	
195 200 205	

141/155

cag gcg tgg ttt ggt ttt gct ggc aca cct gga tat ctt tct cca gaa	672
Gln Ala Trp Phe Gly Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu	
210 215 220	
ggt tta cgt aaa gat cct tat gga aag cca gtg gat atg tgg gca tgt	720
Val Leu Arg Lys Asp Pro Tyr Gly Lys Pro Val Asp Met Trp Ala Cys	
225 230 235 240	
ggt gtc att ctc tat att cta ctt gtg ggg tat cca ccc ttc tgg gat	768
Gly Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp	
245 250 255	
gaa gac caa cac aga ctc tat cag cag atc aag gct gga gct tat gat	816
Glu Asp Gln His Arg Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp	
260 265 270	
ttt cca tca cca gaa tgg gac acg gtg act cct gaa gcc aaa gac ctc	864
Phe Pro Ser Pro Glu Trp Asp Thr Val Thr Pro Glu Ala Lys Asp Leu	
275 280 285	
atc aat aaa atg ctt act atc aac cct gcc aaa cgc atc aca gcc tca	912
Ile Asn Lys Met Leu Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Ser	
290 295 300	
gag gca ctg aag cac cca tgg atc tgt caa cgt tct act gtt gct tcc	960
Glu Ala Leu Lys His Pro Trp Ile Cys Gln Arg Ser Thr Val Ala Ser	
305 310 315 320	
atg atg cac aga cag gag act gta gac tgc ttg aag aaa ttt aat gct	1008
Met Met His Arg Gln Glu Thr Val Asp Cys Leu Lys Lys Phe Asn Ala	
325 330 335	
aga aga aaa cta aag ggt gcc atc ttg aca act atg ctg gct aca agg	1056
Arg Arg Lys Leu Lys Gly Ala Ile Leu Thr Thr Met Leu Ala Thr Arg	
340 345 350	
aat ttc tca ggt aca tgc att ggg aac tct gct tct tat ccc ttg gag	1104
Asn Phe Ser Gly Thr Cys Ile Gly Asn Ser Ala Ser Tyr Pro Leu Glu	
355 360 365	
ccc caa act act gta atc cac aac cct gat gga aac aag gag tca act	1152
Pro Gln Thr Thr Val Ile His Asn Pro Asp Gly Asn Lys Glu Ser Thr	
370 375 380	
gag agt tca aat aca aca att gag gat gaa gat gtg aaa gaa gaa ggt	1200
Glu Ser Ser Asn Thr Thr Ile Glu Asp Glu Asp Val Lys Glu Glu Gly	
385 390 395 400	
ata act aga ata acc aat aca gag aag tgc tta aag gag ctg atg gag	1248
Ile Thr Arg Ile Thr Asn Thr Glu Lys Cys Leu Lys Glu Leu Met Glu	
405 410 415	
ctg aaa acc aag gct caa gaa cta cgt gaa gaa tgc aga agc ctc agg	1296
Leu Lys Thr Lys Ala Gln Glu Leu Arg Glu Glu Cys Arg Ser Leu Arg	
420 425 430	
agc cga tgc gat caa ctg gaa gaa agg gtg tca gtg atg gaa gat gaa	1344
Ser Arg Cys Asp Gln Leu Glu Glu Arg Val Ser Val Met Glu Asp Glu	
435 440 445	

142/155

atg aat gaa atg aag caa gaa ggg aag ttt aga gaa aaa aga ata aaa 1392
 Met Asn Glu Met Lys Gln Glu Gly Lys Phe Arg Glu Lys Arg Ile Lys
 450 455 460

aga aat gag caa agc 1407
 Arg Asn Glu Gln Ser
 465

<210> 74
 <211> 469
 <212> PRT
 <213> Homo sapiens

<400> 74
 Lys Gly Val Gly Arg Phe Lys Asp Arg Lys Tyr Glu Ile Ile Arg Phe
 1 5 10 15
 His Tyr Thr Lys Leu Ser Leu Ala Val Trp Gln Gly Ile Ile Gly
 20 25 30
 Gly Gln Asn Gly Ser Gly Gly Lys Trp Ile Leu Glu Glu Ser Lys Lys
 35 40 45
 Lys Asn Asp Asn Asp Leu Gly Ile Gly Glu Ser Ser Arg Gly Glu Asn
 50 55 60
 Leu Cys Phe Ile Phe Lys Ser Ser Val Arg Val Cys His Val Met Glu
 65 70 75 80
 Val His Ala Tyr Thr Gly Ser His Tyr Val Ala Gln Thr Glu Phe Leu
 85 90 95
 Gly Ser Ser Asp Pro Pro Ala Leu Ala Ser Gln Asn Ala Glu Val Thr
 100 105 110
 Ser Leu Ser His His Thr Tyr Leu Val Ser Pro Cys Ser Asn Lys Ile
 115 120 125
 Tyr Pro Glu Tyr Phe Thr Gly Gly Glu Leu Phe Glu Asp Ile Val Ala
 130 135 140
 Arg Glu Tyr Tyr Ser Glu Ala Asp Ala Ser His Cys Ile Gln Gln Ile
 145 150 155 160
 Leu Glu Ala Val Leu His Cys His Gln Met Gly Val Val His Arg Asp
 165 170 175
 Leu Lys Pro Glu Asn Leu Leu Leu Ala Ser Lys Ser Lys Gly Ala Ala
 180 185 190
 Val Lys Leu Ala Asp Phe Gly Leu Ala Ile Glu Val Gln Gly Asp Gln
 195 200 205
 Gln Ala Trp Phe Gly Phe Ala Gly Thr Pro Gly Tyr Leu Ser Pro Glu
 210 215 220
 Val Leu Arg Lys Asp Pro Tyr Gly Lys Pro Val Asp Met Trp Ala Cys
 225 230 235 240
 Gly Val Ile Leu Tyr Ile Leu Leu Val Gly Tyr Pro Pro Phe Trp Asp
 245 250 255
 Glu Asp Gln His Arg Leu Tyr Gln Gln Ile Lys Ala Gly Ala Tyr Asp
 260 265 270
 Phe Pro Ser Pro Glu Trp Asp Thr Val Thr Pro Glu Ala Lys Asp Leu
 275 280 285
 Ile Asn Lys Met Leu Thr Ile Asn Pro Ala Lys Arg Ile Thr Ala Ser
 290 295 300
 Glu Ala Leu Lys His Pro Trp Ile Cys Gln Arg Ser Thr Val Ala Ser
 305 310 315 320
 Met Met His Arg Gln Glu Thr Val Asp Cys Leu Lys Lys Phe Asn Ala
 325 330 335
 Arg Arg Lys Leu Lys Gly Ala Ile Leu Thr Thr Met Leu Ala Thr Arg
 340 345 350
 Asn Phe Ser Gly Thr Cys Ile Gly Asn Ser Ala Ser Tyr Pro Leu Glu
 355 360 365

143/155

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Pro  Gln Thr  Thr Val  Ile His Asn Pro Asp Gly Asn Lys Glu Ser Thr
    370                375                380
Glu  Ser Ser  Asn Thr  Thr  Ile Glu Asp Glu Asp Val Lys Glu Glu Gly
385                390                395                400
Ile  Thr Arg  Ile  Thr Asn Thr  Glu Lys Cys Leu Lys Glu Leu Met Glu
    405                410                415
Leu  Lys Thr  Lys Ala Gln Glu Leu Arg Glu Glu Cys Arg Ser Leu Arg
    420                425                430
Ser  Arg Cys  Asp Gln Leu Glu Glu Arg Val Ser Val Met Glu Asp Glu
    435                440                445
Met  Asn Glu Met  Lys Gln Glu Gly Lys Phe Arg Glu Lys Arg Ile Lys
    450                455                460
Arg  Asn Glu Gln Ser
465

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<210> 75
<211> 1833
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)...(1833)
<223> MOOSE03376

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<400> 75
atg gag tcg ctg gtt ttc gcg cgg cgc tcc ggc ccc act ccc tcg gcc 48
Met Glu Ser Leu Val Phe Ala Arg Arg Ser Gly Pro Thr Pro Ser Ala
 1                5                10                15

gca gag cta gcc cgg ccg ctg gcg gaa ggg ctg atc aag tcg ccc aag 96
Ala Glu Leu Ala Arg Pro Leu Ala Glu Gly Leu Ile Lys Ser Pro Lys
    20                25                30

ccc cta atg aag aag cag gcg gtg aag cgg cac cac cac aag cac aac 144
Pro Leu Met Lys Lys Gln Ala Val Lys Arg His His His Lys His Asn
    35                40                45

ctg cgg cac cgc tac gag ttc ctg gag acc ctg ggc aaa ggc acc tac 192
Leu Arg His Arg Tyr Glu Phe Leu Glu Thr Leu Gly Lys Gly Thr Tyr
    50                55                60

ggg aag gtg aag aag gcg cgg gag agc tcg ggg cgc ctg gtg gcc atc 240
Gly Lys Val Lys Lys Ala Arg Glu Ser Ser Gly Arg Leu Val Ala Ile
    65                70                75                80

aag tca atc cgg aag gac aaa atc aaa gat gag caa gat ctg atg cac 288
Lys Ser Ile Arg Lys Asp Lys Ile Lys Asp Glu Gln Asp Leu Met His
    85                90                95

ata cgg agg gag att gag atc atg tca tca ctc aac cac cct cac atc 336
Ile Arg Arg Glu Ile Glu Ile Met Ser Ser Leu Asn His Pro His Ile
    100                105                110

att gcc atc cat gaa gtg ttt gag aac agc agc aag atc gtg atc gtc 384
Ile Ala Ile His Glu Val Phe Glu Asn Ser Ser Lys Ile Val Ile Val
    115                120                125

atg gag tat gcc agc cgg ggc gac ctt tat gac tac atc agc gag cgg 432
Met Glu Tyr Ala Ser Arg Gly Asp Leu Tyr Asp Tyr Ile Ser Glu Arg
    130                135                140

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144/155

cag Gln 145	cag Gln 145	ctc Leu 145	agt Ser 145	gag Glu 145	cgc Arg 150	gaa Glu 150	gct Ala 150	agg Arg 150	cat His 150	ttc Phe 155	ttc Phe 155	cgg Arg 155	cag Gln 155	atc Ile 160	gtc Val 160	480
tct Ser 165	gcc Ala 165	gtg Val 165	cac His 165	tat Tyr 165	tgc Cys 165	cat His 165	cag Gln 170	aac Asn 170	aga Arg 170	gtt Val 170	gtc Val 170	cac His 175	cga Arg 175	gat Asp 175	ctc Leu 175	528
aag Lys 180	ctg Leu 180	gag Glu 180	aac Asn 180	atc Ile 180	ctc Leu 180	ttg Leu 180	gat Asp 185	gcc Ala 185	aat Asn 185	ggg Gly 190	aat Asn 190	atc Ile 190	aag Lys 190	att Ile 190	gct Ala 190	576
gac Asp 195	ttc Phe 195	ggg Gly 195	ctc Leu 195	tcc Ser 195	aac Asn 200	ctc Leu 200	tac Tyr 200	cat His 200	caa Gln 205	ggc Gly 205	aag Lys 205	ttc Phe 205	ctg Leu 205	cag Gln 205	aca Thr 205	624
ttc Phe 210	tgt Cys 210	ggg Gly 210	agc Ser 210	ccc Pro 210	ctc Leu 215	tat Tyr 215	gcc Ala 215	tcg Ser 215	cca Pro 220	gag Glu 220	att Ile 220	gtc Val 220	aat Asn 220	ggg Gly 220	aag Lys 220	672
ccc Pro 225	tac Tyr 225	aca Thr 225	ggc Gly 225	cca Pro 230	gag Glu 230	gtg Val 230	gac Asp 230	agc Ser 235	tgg Trp 235	tcc Ser 235	ctg Leu 235	ggg Gly 240	gtt Val 240	ctc Leu 240	ctc Leu 240	720
tac Tyr 245	atc Ile 245	ctg Leu 245	gtg Val 245	cat His 245	ggc Gly 245	acc Thr 245	atg Met 250	ccc Pro 250	ttt Phe 250	gat Asp 250	ggg Gly 255	cat His 255	gac Asp 255	cat His 255	aag Lys 255	768
atc Ile 260	cta Leu 260	gtg Val 260	aaa Lys 260	cag Gln 260	atc Ile 260	agc Ser 265	aac Asn 265	ggg Gly 265	gcc Ala 265	tac Tyr 270	cgg Arg 270	gag Glu 270	cca Pro 270	cct Pro 270	aaa Lys 270	816
ccc Pro 275	tct Ser 275	gca Ala 275	cct Pro 275	gcc Ala 280	ttt Phe 280	tgt Cys 280	ctt Leu 280	cca Pro 285	gat Asp 285	gcc Ala 285	tgt Cys 285	ggc Gly 285	ctg Leu 285	atc Ile 285	cgg Arg 285	864
tgg Trp 290	ctg Leu 290	ttg Leu 290	atg Met 290	gtg Val 295	aac Asn 295	ccc Pro 295	acc Thr 295	cgc Arg 300	cgg Arg 300	gcc Ala 300	acc Thr 300	ctg Leu 300	gag Glu 300	gat Asp 300	gtg Val 300	912
gcc Ala 305	agt Ser 305	cac His 305	tgg Trp 310	tgg Trp 310	gtc Val 310	aac Asn 310	tgg Trp 315	ggc Gly 315	tac Tyr 315	gcc Ala 315	acc Thr 315	cga Arg 315	gtg Val 315	gga Gly 320	gag Glu 320	960
cag Gln 325	gag Glu 325	gct Ala 325	ccg Pro 325	cat His 325	gag Glu 330	ggg Gly 330	ggg Gly 330	cac His 330	cct Pro 330	ggc Gly 335	agt Ser 335	gac Asp 335	tct Ser 335	gcc Ala 335	cgc Arg 335	1008
gcc Ala 340	tcc Ser 340	atg Met 340	gct Ala 340	gac Asp 340	tgg Trp 345	ctc Leu 345	cgg Arg 345	cgt Arg 345	tcc Ser 345	tcc Ser 345	cgc Arg 350	ccc Pro 350	ctc Leu 350	ctg Leu 350	gag Glu 350	1056
aat Asn 355	ggg Gly 355	gcc Ala 355	aag Lys 355	gtg Val 360	tgc Cys 360	agc Ser 360	ttc Phe 360	ttc Phe 360	aag Lys 365	cag Gln 365	cat His 365	gca Ala 365	cct Pro 365	ggg Gly 365	ggg Gly 365	1104
gga Gly 370	agc Ser 370	acc Thr 370	acc Thr 370	cct Pro 375	ggc Gly 375	ctg Leu 375	gag Glu 375	cgc Arg 380	cag Gln 380	cat His 380	tcg Ser 380	ctc Leu 380	aag Lys 380	aag Lys 380	tcc Ser 380	1152

145/155

cgC aag gag aat gac atg gcc cag tct ctc cac agt gac acg gct gat	1200
Arg Lys Glu Asn Asp Met Ala Gln Ser Leu His Ser Asp Thr Ala Asp	
385 390 395 400	
gac act gcc cat cgC cct ggc aag agc aac ctc aag ctg cca aag ggc	1248
Asp Thr Ala His Arg Pro Gly Lys Ser Asn Leu Lys Leu Pro Lys Gly	
405 410 415	
att ctc aag aag aag gtg tca gcc tct gca gaa ggg gta cag gag gac	1296
Ile Leu Lys Lys Lys Val Ser Ala Ser Ala Glu Gly Val Gln Glu Asp	
420 425 430	
cct ccg gag ctc agc cca atc cct gcg agc cca ggg cag gct gcc ccc	1344
Pro Pro Glu Leu Ser Pro Ile Pro Ala Ser Pro Gly Gln Ala Ala Pro	
435 440 445	
ctg ctc ccc aag aag ggc att ctc aag aag ccc cga cag cgc gag tct	1392
Leu Leu Pro Lys Lys Gly Ile Leu Lys Lys Pro Arg Gln Arg Glu Ser	
450 455 460	
ggc tac tac tcc tct ccc gag ccc agt gaa tct ggg gag ctc ttg gac	1440
Gly Tyr Tyr Ser Ser Pro Glu Pro Ser Glu Ser Gly Glu Leu Leu Asp	
465 470 475 480	
gca ggc gac gtg ttt gtg agt ggg gat ccc aag gag cag aag cct ccg	1488
Ala Gly Asp Val Phe Val Ser Gly Asp Pro Lys Glu Gln Lys Pro Pro	
485 490 495	
caa gct tca ggg ctg ctc ctc cat cgC aaa ggc atc ctc aaa ctc aat	1536
Gln Ala Ser Gly Leu Leu Leu His Arg Lys Gly Ile Leu Lys Leu Asn	
500 505 510	
ggc aag ttc tcc cag aca gcc ttg gag ctc gcg gcc ccc acc acc ttc	1584
Gly Lys Phe Ser Gln Thr Ala Leu Glu Leu Ala Ala Pro Thr Thr Phe	
515 520 525	
ggc tcc ctg gat gaa ctc gcc cca cct cgC ccc ctg gcc cgg gcc agc	1632
Gly Ser Leu Asp Glu Leu Ala Pro Pro Arg Pro Leu Ala Arg Ala Ser	
530 535 540	
cga ccc tca ggg gct gtg agc gag gac agc atc ctg tcc tct gag tcc	1680
Arg Pro Ser Gly Ala Val Ser Glu Asp Ser Ile Leu Ser Ser Glu Ser	
545 550 555 560	
ttt gac cag ctg gac ttg cct gaa cgg ctc cca gag ccc cca ctg cgg	1728
Phe Asp Gln Leu Asp Leu Pro Glu Arg Leu Pro Glu Pro Pro Leu Arg	
565 570 575	
ggc tgt gct cat tat acc tcc tgc cac atc tat atc aac agc ccc tgt	1776
Gly Cys Ala His Tyr Thr Ser Cys His Ile Tyr Ile Asn Ser Pro Cys	
580 585 590	
acc cca aca tct aac cag aag ccc cga ctt cac agg gtc agt gga gaa	1824
Thr Pro Thr Ser Asn Gln Lys Pro Arg Leu His Arg Val Ser Gly Glu	
595 600 605	
tca ata aaa	1833
Ser Ile Lys	
610	

146/155

<211> 611

<212> PRT

<213> Homo sapiens

<400> 76

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Met Glu Ser Leu Val Phe Ala Arg Arg Ser Gly Pro Thr Pro Ser Ala
 1      5      10      15
Ala Glu Leu Ala Arg Pro Leu Ala Glu Leu Ile Lys Ser Pro Lys
      20      25      30
Pro Leu Met Lys Lys Gln Ala Val Lys Arg His His His Lys His Asn
      35      40      45
Leu Arg His Arg Tyr Glu Phe Leu Glu Thr Leu Gly Lys Gly Thr Tyr
      50      55      60
Gly Lys Val Lys Lys Ala Arg Glu Ser Ser Gly Arg Leu Val Ala Ile
      65      70      75      80
Lys Ser Ile Arg Lys Asp Lys Ile Lys Asp Glu Gln Asp Leu Met His
      85      90      95
Ile Arg Arg Glu Ile Glu Ile Met Ser Ser Leu Asn His Pro His Ile
      100      105      110
Ile Ala Ile His Glu Val Phe Glu Asn Ser Ser Lys Ile Val Ile Val
      115      120      125
Met Glu Tyr Ala Ser Arg Gly Asp Leu Tyr Asp Tyr Ile Ser Glu Arg
      130      135      140
Gln Gln Leu Ser Glu Arg Glu Ala Arg His Phe Phe Arg Gln Ile Val
      145      150      155      160
Ser Ala Val His Tyr Cys His Gln Asn Arg Val Val His Arg Asp Leu
      165      170      175
Lys Leu Glu Asn Ile Leu Leu Asp Ala Asn Gly Asn Ile Lys Ile Ala
      180      185      190
Asp Phe Gly Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr
      195      200      205
Phe Cys Gly Ser Pro Leu Tyr Ala Ser Pro Glu Ile Val Asn Gly Lys
      210      215      220
Pro Tyr Thr Gly Pro Glu Val Asp Ser Trp Ser Leu Gly Val Leu Leu
      225      230      235      240
Tyr Ile Leu Val His Gly Thr Met Pro Phe Asp Gly His Asp His Lys
      245      250      255
Ile Leu Val Lys Gln Ile Ser Asn Gly Ala Tyr Arg Glu Pro Pro Lys
      260      265      270
Pro Ser Ala Pro Ala Phe Cys Leu Pro Asp Ala Cys Gly Leu Ile Arg
      275      280      285
Trp Leu Leu Met Val Asn Pro Thr Arg Arg Ala Thr Leu Glu Asp Val
      290      295      300
Ala Ser His Trp Trp Val Asn Trp Gly Tyr Ala Thr Arg Val Gly Glu
      305      310      315      320
Gln Glu Ala Pro His Glu Gly Gly His Pro Gly Ser Asp Ser Ala Arg
      325      330      335
Ala Ser Met Ala Asp Trp Leu Arg Arg Ser Ser Arg Pro Leu Leu Glu
      340      345      350
Asn Gly Ala Lys Val Cys Ser Phe Phe Lys Gln His Ala Pro Gly Gly
      355      360      365
Gly Ser Thr Thr Pro Gly Leu Glu Arg Gln His Ser Leu Lys Lys Ser
      370      375      380
Arg Lys Glu Asn Asp Met Ala Gln Ser Leu His Ser Asp Thr Ala Asp
      385      390      395      400
Asp Thr Ala His Arg Pro Gly Lys Ser Asn Leu Lys Leu Pro Lys Gly
      405      410      415
Ile Leu Lys Lys Lys Val Ser Ala Ser Ala Glu Gly Val Gln Glu Asp
      420      425      430
Pro Pro Glu Leu Ser Pro Ile Pro Ala Ser Pro Gly Gln Ala Ala Pro
      435      440      445

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147/155

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Leu Leu Pro Lys Lys Gly Ile Leu Lys Lys Pro Arg Gln Arg Glu Ser
  450      455      460
Gly Tyr Tyr Ser Ser Pro Glu Pro Ser Glu Ser Gly Glu Leu Leu Asp
465      470      475      480
Ala Gly Asp Val Phe Val Ser Gly Asp Pro Lys Glu Gln Lys Pro Pro
      485      490      495
Gln Ala Ser Gly Leu Leu Leu His Arg Lys Gly Ile Leu Lys Leu Asn
      500      505      510
Gly Lys Phe Ser Gln Thr Ala Leu Glu Leu Ala Ala Pro Thr Thr Phe
      515      520      525
Gly Ser Leu Asp Glu Leu Ala Pro Pro Arg Pro Leu Ala Arg Ala Ser
      530      535      540
Arg Pro Ser Gly Ala Val Ser Glu Asp Ser Ile Leu Ser Ser Glu Ser
545      550      555      560
Phe Asp Gln Leu Asp Leu Pro Glu Arg Leu Pro Glu Pro Pro Leu Arg
      565      570      575
Gly Cys Ala His Tyr Thr Ser Cys His Ile Tyr Ile Asn Ser Pro Cys
      580      585      590
Thr Pro Thr Ser Asn Gln Lys Pro Arg Leu His Arg Val Ser Gly Glu
      595      600      605
Ser Ile Lys
      610

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<210> 77
 <211> 2346
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(2346)
 <223> MOOSE03459

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<400> 77
atg atc act tat act ttg ata aaa tca tca ctt att aca ccc caa aat   48
Met Ile Thr Tyr Thr Leu Ile Lys Ser Ser Leu Ile Thr Pro Gln Asn
  1      5      10      15

tct gga gtc atc ttt gac tcc ccc att cag gca aga agt cat gtt ggc   96
Ser Gly Val Ile Phe Asp Ser Pro Ile Gln Ala Arg Ser His Val Gly
      20      25      30

tct acc ttc aaa ata tat cca aaa tca agc att tct tct tgc ctc tgt   144
Ser Thr Phe Lys Ile Tyr Pro Lys Ser Ser Ile Ser Ser Cys Leu Cys
      35      40      45

tct tac cac tct ggt ccc agc tgc ctt cat ctt tta tct gga tca ttc   192
Ser Tyr His Ser Gly Pro Ser Cys Leu His Leu Leu Ser Gly Ser Phe
      50      55      60

cag gag tcc tca aat tct tat cat tcc ctc tcc cct tgc ctc cct aca   240
Gln Glu Ser Ser Asn Ser Tyr His Ser Leu Ser Pro Cys Leu Pro Thr
      65      70      75      80

atc tgt tgt cag cac aac agc cac atc ctt tcc ttg cag gct tct ttt   288
Ile Cys Cys Gln His Asn Ser His Ile Leu Ser Leu Gln Ala Ser Phe
      85      90      95

att gtg ttt gat tct cct aga aat ttc tct gat tct cct agt cat tcc   336
Ile Val Phe Asp Ser Pro Arg Asn Phe Ser Asp Ser Pro Ser His Ser
      100      105      110

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148/155

aaa gca aag agc ccc atg gag agg aga gcc gca ccc aga acc aag cta	384
Lys Ala Lys Ser Pro Met Glu Arg Arg Ala Ala Pro Arg Thr Lys Leu	
115 120 125	
gag gtt tac gga ggt ctc ctc tct tcc ctg tct tcc tca ctt gtt gcc	432
Glu Val Tyr Gly Gly Leu Ser Ser Leu Ser Ser Ser Leu Val Ala	
130 135 140	
cct gtc att cgc tct gct cca gct aca cgg gct tcc ttg ctg ttc cct	480
Pro Val Ile Arg Ser Ala Pro Ala Thr Arg Ala Ser Leu Leu Phe Pro	
145 150 155 160	
gct gtc aga cat gtt ccc cca gca cca cct gaa ggc ctc cgc ccc agt	528
Ala Val Arg His Val Pro Pro Ala Pro Pro Glu Gly Leu Arg Pro Ser	
165 170 175	
aga agc tgc agt tct tct gtg atc cta gga aga gag aac aga tgc tca	576
Arg Ser Cys Ser Ser Ser Val Ile Leu Gly Arg Glu Asn Arg Cys Ser	
180 185 190	
caa gcc cca ccc agt gag cag cag aag aca agc act ctg aga cca cac	624
Gln Ala Pro Pro Ser Glu Gln Gln Lys Thr Ser Thr Leu Arg Pro His	
195 200 205	
ttt agg cca ccg gtg gga cca aaa ggg aac agg tgc ctc agc cat ccc	672
Phe Arg Pro Pro Val Gly Pro Lys Gly Asn Arg Cys Leu Ser His Pro	
210 215 220	
aac agt gtc gtc aga ggg tcc cca ggg cat ttt cat ggc aag tac ccc	720
Asn Ser Val Val Arg Gly Ser Pro Gly His Phe His Gly Lys Tyr Pro	
225 230 235 240	
tct gcc ccc act cca gca gtg ctt ccc aaa gtg aag cag agc tgg cag	768
Ser Ala Pro Thr Pro Ala Val Leu Pro Lys Val Lys Gln Ser Trp Gln	
245 250 255	
gcc tta gct aca ggc tct ctc tca ggc aga tcc ctt tta aga tac ata	816
Ala Leu Ala Thr Gly Ser Leu Ser Gly Arg Ser Leu Leu Arg Tyr Ile	
260 265 270	
cac cat gcc cac aca tcc cat gga gag aga cca atg ctt tat tct aac	864
His His Ala His Thr Ser His Gly Glu Arg Pro Met Leu Tyr Ser Asn	
275 280 285	
tgg tca cag ggt cac cca cct agt agt gat gct tcc cag gct act ttg	912
Trp Ser Gln Gly His Pro Pro Ser Ser Asp Ala Ser Gln Ala Thr Leu	
290 295 300	
ctg atg ctg cgt ttg ctt ctg tca ttc tgc tca acc act tcc aaa tct	960
Leu Met Leu Arg Leu Leu Leu Ser Phe Cys Ser Thr Thr Ser Lys Ser	
305 310 315 320	
gct ttt tgt agc ctc act tct ctg cat gtt ttt tta acc ttc cac cct	1008
Ala Phe Cys Ser Leu Thr Ser Leu His Val Phe Leu Thr Phe His Pro	
325 330 335	
cat ttc ctt atc ttg tcc cgg gag ccc ggg gcc ggc cct ggt gcg ggg	1056
His Phe Leu Ile Leu Ser Arg Glu Pro Gly Ala Gly Pro Gly Ala Gly	
340 345 350	

149/155

tgc Cys	ggg Gly	gcc Ala	ggg Gly	agg Arg	gca Ala	ggt Gly	gcg Ala	cgc Arg	gca Ala	gcg Ala	agc Ser	ccc Pro	tcc Ser	ccc Pro	gcg Ala	1104
		355					360					365				
ccc Pro	cca Pro	aag Lys	ctc Leu	ggg Gly	ggc Gly	acc Thr	ccg Pro	acc Thr	ctc Leu	ccc Pro	acg Thr	cgc Arg	ctg Leu	gcc Ala	ccg Pro	1152
		370				375					380					
gcg Ala	cgg Arg	ccc Pro	tca Ser	ccc Pro	gag Glu	cgg Arg	ggg Gly	tcg Ser	aag Lys	gtg Val	acc Thr	acg Thr	aac Asn	acg Thr	gcc Ala	1200
					390					395					400	
acc Thr	acc Thr	tgg Trp	tcc Ser	tcc Ser	tcc Ser	acc Thr	att Ile	tgt Cys	ggg Gly	acg Thr	agg Arg	gat Asp	att Ile	ccc Pro	tca Ser	1248
					405				410					415		
gaa Glu	gat Asp	cag Gln	gaa Glu	aag Lys	gaa Glu	cta Leu	ttc Phe	ctt Leu	atg Met	gaa Glu	tta Leu	ttt Phe	gcc Ala	ctc Leu	tct Ser	1296
			420					425					430			
aga Arg	gca Ala	cat His	tta Leu	tac Tyr	tct Ser	caa Gln	cct Pro	gtg Val	tca Ser	tct Ser	ttc Phe	aat Asn	aaa Lys	ttt Phe	tca Ser	1344
		435					440					445				
aat Asn	tcc Ser	tct Ser	gct Ala	tcc Ser	aag Lys	cag Gln	aaa Lys	tgt Cys	gtt Val	tta Leu	cga Arg	gaa Glu	acc Thr	aac Asn	atg Met	1392
	450					455					460					
gct Ala	tcc Ser	cgc Arg	tat Tyr	gaa Glu	aaa Lys	gaa Glu	ttc Phe	ttg Leu	gag Glu	gtt Val	gaa Glu	aaa Lys	att Ile	ggg Gly	gtt Val	1440
	465				470				475						480	
ggc Gly	gaa Glu	ttt Phe	ggt Gly	aca Thr	gtc Val	tac Tyr	aag Lys	tgc Cys	att Ile	aag Lys	agg Arg	ctg Leu	gat Asp	gga Gly	tgt Cys	1488
				485					490					495		
gtt Val	tat Tyr	gca Ala	ata Ile	aag Lys	cgc Arg	tct Ser	atg Met	aaa Lys	act Thr	ttt Phe	aca Thr	gaa Glu	tta Leu	tca Ser	aat Asn	1536
			500					505					510			
gag Glu	aat Asn	tcg Ser	gct Ala	ttg Leu	cat His	gaa Glu	gtt Val	tat Tyr	gct Ala	cac His	gca Ala	gtg Val	ctt Leu	ggg Gly	cat His	1584
		515					520					525				
cac His	ccc Pro	cat His	gtg Val	gta Val	cgt Arg	tac Tyr	tat Tyr	tcc Ser	tca Ser	tgg Trp	gca Ala	gaa Glu	gat Asp	gac Asp	cac His	1632
	530					535					540					
atg Met	atc Ile	att Ile	cag Gln	aat Asn	gaa Glu	tac Tyr	tgc Cys	aat Asn	ggt Gly	ggg Gly	agt Ser	ttg Leu	caa Gln	gct Ala	gct Ala	1680
	545				550				555						560	
ata Ile	tct Ser	gaa Glu	aac Asn	act Thr	aag Lys	tct Ser	ggc Gly	aat Asn	cat His	ttt Phe	gaa Glu	gag Glu	cca Pro	aaa Lys	ctc Leu	1728
				565				570						575		
aag Lys	gac Asp	atc Ile	ctt Leu	cta Leu	cag Gln	att Ile	tcc Ser	ctt Leu	ggc Gly	ctt Leu	aat Asn	tac Tyr	atc Ile	cac His	aac Asn	1776
			580					585					590			

150/155

tct agc atg gta cac ctg gac atc aaa cct agt aat ata ttc att tgt	1824
Ser Ser Met Val His Leu Asp Ile Lys Pro Ser Asn Ile Phe Ile Cys	
595 600 605	
cac aag atg caa agt gaa tcc tct gga gtc ata gaa gaa gtt gaa aat	1872
His Lys Met Gln Ser Glu Ser Ser Gly Val Ile Glu Glu Val Glu Asn	
610 615 620	
gaa gct gat tgg ttt ctc tct gcc aat gtg atg tat aaa att ggt gac	1920
Glu Ala Asp Trp Phe Leu Ser Ala Asn Val Met Tyr Lys Ile Gly Asp	
625 630 635 640	
ctg ggc cac gca aca tca ata aac aaa ccc aaa gtg gaa gaa gga gat	1968
Leu Gly His Ala Thr Ser Ile Asn Lys Pro Lys Val Glu Glu Gly Asp	
645 650 655	
agt cgc ttc ctg gct aat gag att ttg caa gag gat tac cgg cac ctt	2016
Ser Arg Phe Leu Ala Asn Glu Ile Leu Gln Glu Asp Tyr Arg His Leu	
660 665 670	
ccc aaa gca gac ata ttt gcc ttg gga tta aca att gca gtg gct gca	2064
Pro Lys Ala Asp Ile Phe Ala Leu Gly Leu Thr Ile Ala Val Ala Ala	
675 680 685	
gga gca gag tca ttg ccc acc aat ggt gct gca tgg cac cat atc cgc	2112
Gly Ala Glu Ser Leu Pro Thr Asn Gly Ala Ala Trp His His Ile Arg	
690 695 700	
aag ggt aac ttt ccg gac gtt cct cag gag ctc tca gaa agc ttt tcc	2160
Lys Gly Asn Phe Pro Asp Val Pro Gln Glu Leu Ser Glu Ser Phe Ser	
705 710 715 720	
agt ctg ctc aag aac atg atc caa cct gat gcc gaa cag aga cct tct	2208
Ser Leu Leu Lys Asn Met Ile Gln Pro Asp Ala Glu Gln Arg Pro Ser	
725 730 735	
gca gca gct ctg gcc aga aat aca gtt ctc cgg cct tcc ctg gga aaa	2256
Ala Ala Ala Leu Ala Arg Asn Thr Val Leu Arg Pro Ser Leu Gly Lys	
740 745 750	
aca gaa gag ctc caa cag cag ctg aat ttg gaa aag ttc aag act gcc	2304
Thr Glu Glu Leu Gln Gln Gln Leu Asn Leu Glu Lys Phe Lys Thr Ala	
755 760 765	
aca ctg gaa agc agt gtt ctg aag gca ttt ttg agt aat tat	2346
Thr Leu Glu Ser Ser Val Leu Lys Ala Phe Leu Ser Asn Tyr	
770 775 780	

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<211> 782

<212> PRT

<213> Homo sapiens

<400> 78

Met Ile Thr Tyr Thr Leu Ile Lys Ser Ser Leu Ile Thr Pro Gln Asn	
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Ser Gly Val Ile Phe Asp Ser Pro Ile Gln Ala Arg Ser His Val Gly	
20 25 30	
Ser Thr Phe Lys Ile Tyr Pro Lys Ser Ser Ile Ser Ser Cys Leu Cys	
35 40 45	

151/155

Ser	Tyr	His	Ser	Gly	Pro	Ser	Cys	Leu	His	Leu	Leu	Ser	Gly	Ser	Phe
50						55					60				
Gln	Glu	Ser	Ser	Asn	Ser	Tyr	His	Ser	Leu	Ser	Pro	Cys	Leu	Pro	Thr
65				70						75					80
Ile	Cys	Cys	Gln	His	Asn	Ser	His	Ile	Leu	Ser	Leu	Gln	Ala	Ser	Phe
			85						90					95	
Ile	Val	Phe	Asp	Ser	Pro	Arg	Asn	Phe	Ser	Asp	Ser	Pro	Ser	His	Ser
			100					105					110		
Lys	Ala	Lys	Ser	Pro	Met	Glu	Arg	Arg	Ala	Ala	Pro	Arg	Thr	Lys	Leu
		115					120					125			
Glu	Val	Tyr	Gly	Gly	Leu	Leu	Ser	Ser	Leu	Ser	Ser	Ser	Leu	Val	Ala
130						135					140				
Pro	Val	Ile	Arg	Ser	Ala	Pro	Ala	Thr	Arg	Ala	Ser	Leu	Leu	Phe	Pro
145					150					155					160
Ala	Val	Arg	His	Val	Pro	Pro	Ala	Pro	Pro	Glu	Gly	Leu	Arg	Pro	Ser
				165					170					175	
Arg	Ser	Cys	Ser	Ser	Ser	Val	Ile	Leu	Gly	Arg	Glu	Asn	Arg	Cys	Ser
			180					185				190			
Gln	Ala	Pro	Pro	Ser	Glu	Gln	Gln	Lys	Thr	Ser	Thr	Leu	Arg	Pro	His
		195					200					205			
Phe	Arg	Pro	Pro	Val	Gly	Pro	Lys	Gly	Asn	Arg	Cys	Leu	Ser	His	Pro
210						215					220				
Asn	Ser	Val	Val	Arg	Gly	Ser	Pro	Gly	His	Phe	His	Gly	Lys	Tyr	Pro
225					230					235					240
Ser	Ala	Pro	Thr	Pro	Ala	Val	Leu	Pro	Lys	Val	Lys	Gln	Ser	Trp	Gln
				245					250					255	
Ala	Leu	Ala	Thr	Gly	Ser	Leu	Ser	Gly	Arg	Ser	Leu	Leu	Arg	Tyr	Ile
			260					265					270		
His	His	Ala	His	Thr	Ser	His	Gly	Glu	Arg	Pro	Met	Leu	Tyr	Ser	Asn
		275					280					285			
Trp	Ser	Gln	Gly	His	Pro	Pro	Ser	Ser	Asp	Ala	Ser	Gln	Ala	Thr	Leu
290						295					300				
Leu	Met	Leu	Arg	Leu	Leu	Leu	Ser	Phe	Cys	Ser	Thr	Thr	Ser	Lys	Ser
305					310					315					320
Ala	Phe	Cys	Ser	Leu	Thr	Ser	Leu	His	Val	Phe	Leu	Thr	Phe	His	Pro
				325					330					335	
His	Phe	Leu	Ile	Leu	Ser	Arg	Glu	Pro	Gly	Ala	Gly	Pro	Gly	Ala	Gly
			340					345					350		
Cys	Gly	Ala	Gly	Arg	Ala	Gly	Ala	Arg	Ala	Ala	Ser	Pro	Ser	Pro	Ala
		355					360					365			
Pro	Pro	Lys	Leu	Gly	Gly	Thr	Pro	Thr	Leu	Pro	Thr	Arg	Leu	Ala	Pro
		370				375						380			
Ala	Arg	Pro	Ser	Pro	Glu	Arg	Gly	Ser	Lys	Val	Thr	Thr	Asn	Thr	Ala
385					390					395					400
Thr	Thr	Trp	Ser	Ser	Ser	Thr	Ile	Cys	Gly	Thr	Arg	Asp	Ile	Pro	Ser
				405					410					415	
Glu	Asp	Gln	Glu	Lys	Glu	Leu	Phe	Leu	Met	Glu	Leu	Phe	Ala	Leu	Ser
			420					425					430		
Arg	Ala	His	Leu	Tyr	Ser	Gln	Pro	Val	Ser	Ser	Phe	Asn	Lys	Phe	Ser
		435					440					445			
Asn	Ser	Ser	Ala	Ser	Lys	Gln	Lys	Cys	Val	Leu	Arg	Glu	Thr	Asn	Met
		450				455					460				
Ala	Ser	Arg	Tyr	Glu	Lys	Glu	Phe	Leu	Glu	Val	Glu	Lys	Ile	Gly	Val
465					470					475					480
Gly	Glu	Phe	Gly	Thr	Val	Tyr	Lys	Cys	Ile	Lys	Arg	Leu	Asp	Gly	Cys
			485						490					495	
Val	Tyr	Ala	Ile	Lys	Arg	Ser	Met	Lys	Thr	Phe	Thr	Glu	Leu	Ser	Asn
			500					505					510		
Glu	Asn	Ser	Ala	Leu	His	Glu	Val	Tyr	Ala	His	Ala	Val	Leu	Gly	His
		515					520					525			
His	Pro	His	Val	Val	Arg	Tyr	Tyr	Ser	Ser	Trp	Ala	Glu	Asp	Asp	His
						535					540				

152/155

Met Ile Ile Gln Asn Glu Tyr Cys Asn Gly Gly Ser Leu Gln Ala Ala
 545 550 555 560
 Ile Ser Glu Asn Thr Lys Ser Gly Asn His Phe Glu Glu Pro Lys Leu
 565 570 575
 Lys Asp Ile Leu Leu Gln Ile Ser Leu Gly Leu Asn Tyr Ile His Asn
 580 585 590
 Ser Ser Met Val His Leu Asp Ile Lys Pro Ser Asn Ile Phe Ile Cys
 595 600 605
 His Lys Met Gln Ser Glu Ser Ser Gly Val Ile Glu Glu Val Glu Asn
 610 615 620
 Glu Ala Asp Trp Phe Leu Ser Ala Asn Val Met Tyr Lys Ile Gly Asp
 625 630 635 640
 Leu Gly His Ala Thr Ser Ile Asn Lys Pro Lys Val Glu Glu Gly Asp
 645 650 655
 Ser Arg Phe Leu Ala Asn Glu Ile Leu Gln Glu Asp Tyr Arg His Leu
 660 665 670
 Pro Lys Ala Asp Ile Phe Ala Leu Gly Leu Thr Ile Ala Val Ala Ala
 675 680 685
 Gly Ala Glu Ser Leu Pro Thr Asn Gly Ala Ala Trp His His Ile Arg
 690 695 700
 Lys Gly Asn Phe Pro Asp Val Pro Gln Glu Leu Ser Glu Ser Phe Ser
 705 710 715 720
 Ser Leu Leu Lys Asn Met Ile Gln Pro Asp Ala Glu Gln Arg Pro Ser
 725 730 735
 Ala Ala Ala Leu Ala Arg Asn Thr Val Leu Arg Pro Ser Leu Gly Lys
 740 745 750
 Thr Glu Glu Leu Gln Gln Gln Leu Asn Leu Glu Lys Phe Lys Thr Ala
 755 760 765
 Thr Leu Glu Ser Ser Val Leu Lys Ala Phe Leu Ser Asn Tyr
 770 775 780

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 <212> DNA
 <213> Homo sapiens

<220>
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 <223> MOOSE03283

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 Leu Ile Asp Leu Asn Gly Phe Leu Met Pro Ser Ile Leu Ser Leu Lys
 1 5 10 15
 aaa tat ttc atg gag cat ttt aca ctg gtg cag agg ata cac gag act 96
 Lys Tyr Phe Met Glu His Phe Thr Leu Val Gln Arg Ile His Glu Thr
 20 25 30
 ctg tct caa aaa aca aaa aca aaa caa aaa aaa aaa caa aaa aaa aaa 144
 Leu Ser Gln Lys Thr Lys Thr Lys Gln Lys Lys Lys Lys Gln Lys Lys Lys
 35 40 45
 aaa aaa aaa aaa aga tcg tcg atg tat gaa gtt aga agc aac cag acc 192
 Lys Lys Lys Lys Arg Ser Ser Met Tyr Glu Val Arg Ser Asn Gln Thr
 50 55 60
 acc tca cat gtc tgt tac tac tta tgt tcc cca tat tgt tct atc aca 240
 Thr Ser His Val Cys Tyr Tyr Leu Cys Ser Pro Tyr Cys Ser Ile Thr
 65 70 75 80

153/155

ctt	agg	act	ttg	atg	cac	aga	tgt	ttg	gtg	gga	gtg	aaa	atg	gtt	gct	288
Leu	Arg	Thr	Leu	Met	His	Arg	Cys	Leu	Val	Gly	Val	Lys	Met	Val	Ala	
				85					90					95		
gat	gga	gtg	atc	aaa	agc	gta	tta	tgg	caa	aca	ctt	caa	gct	ctt	aat	336
Asp	Gly	Val	Ile	Lys	Ser	Val	Leu	Trp	Gln	Thr	Leu	Gln	Ala	Leu	Asn	
			100					105					110			
ttc	tgt	cat	ata	cat	aac	tgt	att	cac	aga	gat	ata	aaa	cct	gaa	aat	384
Phe	Cys	His	Ile	His	Asn	Cys	Ile	His	Arg	Asp	Ile	Lys	Pro	Glu	Asn	
		115					120					125				
att	cta	ata	act	aag	caa	gga	ata	atc	aag	att	tgt	gac	ttc	ggg	ttt	432
Ile	Leu	Ile	Thr	Lys	Gln	Gly	Ile	Ile	Lys	Ile	Cys	Asp	Phe	Gly	Phe	
	130					135					140					
gca	caa	att	ctg	att	cca	gga	gat	gcc	tac	acc	gat	tat	gta	gct	acg	480
Ala	Gln	Ile	Leu	Ile	Pro	Gly	Asp	Ala	Tyr	Thr	Asp	Tyr	Val	Ala	Thr	
145					150				155						160	
aga	tgg	tac	cga	gct	cct	gaa	ctt	ctt	gtg	gga	gat	act	cag	tat	ggg	528
Arg	Trp	Tyr	Arg	Ala	Pro	Glu	Leu	Leu	Val	Gly	Asp	Thr	Gln	Tyr	Gly	
				165					170					175		
tct	tca	gtc	gat	ata	tgg	gct	att	ggg	tgt	gtt	ttt	gca	gag	ctc	ctg	576
Ser	Ser	Val	Asp	Ile	Trp	Ala	Ile	Gly	Cys	Val	Phe	Ala	Glu	Leu	Leu	
			180					185					190			
aca	ggc	cag	cca	ctg	tgg	cct	gga	aaa	tca	gat	gtg	gac	caa	ctt	tat	624
Thr	Gly	Gln	Pro	Leu	Trp	Pro	Gly	Lys	Ser	Asp	Val	Asp	Gln	Leu	Tyr	
		195					200					205				
ctg	ata	atc	aga	aca	cta	gga	aaa	tta	atc	cca	aga	cat	caa	tca	atc	672
Leu	Ile	Ile	Arg	Thr	Leu	Gly	Lys	Leu	Ile	Pro	Arg	His	Gln	Ser	Ile	
	210					215					220					
ttt	aaa	agt	aac	ggg	ttt	ttc	cat	ggc	atc	agt	ata	cct	gag	cca	gaa	720
Phe	Lys	Ser	Asn	Gly	Phe	Phe	His	Gly	Ile	Ser	Ile	Pro	Glu	Pro	Glu	
225				230					235						240	
gac	atg	gaa	act	ctt	gag	gaa	aag	ttc	tca	gat	gtt	cat	cct	gtg	gct	768
Asp	Met	Glu	Thr	Leu	Glu	Glu	Lys	Phe	Ser	Asp	Val	His	Pro	Val	Ala	
				245					250					255		
ctg	aac	ttc	atg	aag	tta	tta	atc	cag	gca	ggc	aag	gac	tca	gaa	gcc	816
Leu	Asn	Phe	Met	Lys	Leu	Leu	Ile	Gln	Ala	Gly	Lys	Asp	Ser	Glu	Ala	
			260					265					270			
tca	att	cta	ctc	agc	tca	tct	caa	tgc	ttc	aga	att	aag	cag	gac	att	864
Ser	Ile	Leu	Leu	Ser	Ser	Ser	Gln	Cys	Phe	Arg	Ile	Lys	Gln	Asp	Ile	
		275					280					285				
gct	gag	gca	gaa	gaa	ttg	ctt	gaa	cct	ggg	agt	ttc	atg	tca	cca	aat	912
Ala	Glu	Ala	Glu	Glu	Leu	Leu	Glu	Pro	Gly	Ser	Phe	Met	Ser	Pro	Asn	
	290					295					300					
gaa	att	gtt	tat	ccg	atc	ttc	caa	gaa	atc	agg	aga	gag	aga	gag	aat	960
Glu	Ile	Val	Tyr	Pro	Ile	Phe	Gln	Glu	Ile	Arg	Arg	Glu	Arg	Glu	Asn	
305					310					315					320	

154/155

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agc caa atc cct aaa cag gcc agt gat cca cct gcc ttg gcc tcc caa 1008
Ser Gln Ile Pro Lys Gln Ala Ser Asp Pro Pro Ala Leu Ala Ser Gln
      325      330      335

cat gct agg att aca ggt gtg agc cat cgc aca cag cca act ctt ttc 1056
His Ala Arg Ile Thr Gly Val Ser His Arg Thr Gln Pro Thr Leu Phe
      340      345      350

ttg aag cat tcc tct ctc aac ttc tca gac 1086
Leu Lys His Ser Ser Leu Asn Phe Ser Asp
      355      360

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<211> 362
<212> PRT
<213> Homo sapiens

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Lys Tyr Phe Met Glu His Phe Thr Leu Val Gln Arg Ile His Glu Thr
      20      25      30
Leu Ser Gln Lys Thr Lys Thr Lys Gln Lys Lys Lys Gln Lys Lys Lys
      35      40      45
Lys Lys Lys Lys Arg Ser Ser Met Tyr Glu Val Arg Ser Asn Gln Thr
      50      55      60
Thr Ser His Val Cys Tyr Tyr Leu Cys Ser Pro Tyr Cys Ser Ile Thr
      65      70      75      80
Leu Arg Thr Leu Met His Arg Cys Leu Val Gly Val Lys Met Val Ala
      85      90      95
Asp Gly Val Ile Lys Ser Val Leu Trp Gln Thr Leu Gln Ala Leu Asn
      100      105      110
Phe Cys His Ile His Asn Cys Ile His Arg Asp Ile Lys Pro Glu Asn
      115      120      125
Ile Leu Ile Thr Lys Gln Gly Ile Ile Lys Ile Cys Asp Phe Gly Phe
      130      135      140
Ala Gln Ile Leu Ile Pro Gly Asp Ala Tyr Thr Asp Tyr Val Ala Thr
      145      150      155      160
Arg Trp Tyr Arg Ala Pro Glu Leu Leu Val Gly Asp Thr Gln Tyr Gly
      165      170      175
Ser Ser Val Asp Ile Trp Ala Ile Gly Cys Val Phe Ala Glu Leu Leu
      180      185      190
Thr Gly Gln Pro Leu Trp Pro Gly Lys Ser Asp Val Asp Gln Leu Tyr
      195      200      205
Leu Ile Ile Arg Thr Leu Gly Lys Leu Ile Pro Arg His Gln Ser Ile
      210      215      220
Phe Lys Ser Asn Gly Phe Phe His Gly Ile Ser Ile Pro Glu Pro Glu
      225      230      235      240
Asp Met Glu Thr Leu Glu Glu Lys Phe Ser Asp Val His Pro Val Ala
      245      250      255
Leu Asn Phe Met Lys Leu Leu Ile Gln Ala Gly Lys Asp Ser Glu Ala
      260      265      270
Ser Ile Leu Leu Ser Ser Ser Gln Cys Phe Arg Ile Lys Gln Asp Ile
      275      280      285
Ala Glu Ala Glu Glu Leu Leu Glu Pro Gly Ser Phe Met Ser Pro Asn
      290      295      300
Glu Ile Val Tyr Pro Ile Phe Gln Glu Ile Arg Arg Glu Arg Glu Asn
      305      310      315      320
Ser Gln Ile Pro Lys Gln Ala Ser Asp Pro Pro Ala Leu Ala Ser Gln
      325      330      335

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155/155

His Ala Arg Ile Thr Gly Val Ser His Arg Thr Gln Pro Thr Leu Phe
340 345 350
Leu Lys His Ser Ser Leu Asn Phe Ser Asp
355 360